GEORG-AUGUST-UNIVERSITÄT
GÖTTINGEN / GERMANY

International Max Planck Research School

Molecular Biology

MSc/PhD Program

YEARBOOK 2015 / 2016

Yearbook 2015/2016

MSc/PhD Molecular Biology Program

at the University of Göttingen

International Max Planck Research School

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Letter from the President

Success for a comprehensive research university such as our Georg-August University of Göttingen is rooted in excellent science and its integration into an optimal learning environment to educate competent and critical young academics. I am very glad that our university in cooperation with the local Max-Planck Institutes and the German Primate Center has been able to establish conditions, which make top interdisciplinary science possible in an international setting enabling us all to feel the Göttingen Spirit.

The two international MSc/PhD programs in Molecular Biology and Neurosciences truly have contributed to our continued strive for excellence in science-oriented training both by integrating faculty members from university and non-university institutes across institutional borders and by providing comprehensive services especially for international students on the Göttingen Campus. Based on the proven concepts and the experience of these programs the Göttingen Graduate School for Neurosciences, Biophysics, and Molecular Biosciences (GGNB) was established, which is continuously supported by the federal Excellence Initiative since 2007.

The Molecular Biology and Neuroscience programs remain unique within the Graduate School GGNB in offering integrated MSc/PhD curricula with a fast track option which allow excellent BSc graduates to directly enter the PhD phase after successfully absolving the initial 1st year training phase. For over a decade these international programs have been particularly successful in attracting high numbers of worldwide applicants of good academic quality providing the basis for the selection of the very best candidates. New ideas introduced by these programs have meanwhile been adopted by the Georg-August University School of Science (GAUSS) and other graduate schools for the benefit of the entire university.

While maintaining their successful structure the content and focus of the training curriculum of the programs has continuously been adapted to the changing research topics. Consequently, new faculty members are integrated to reflect novel developments in research. They will further ensure optimal individual supervision and up-to-date research-oriented training. Beyond academia both programs keep close contact with the relevant industries to enhance the opportunities of the graduates for a successful professional career in the private sector.

I would very much like to thank all colleagues and institutions for their committed support of these international programs and, last but not least, the German Academic Exchange Service (DAAD), the Lower Saxony Ministry of Science and Culture, and the various generous donors. The Georg-August University of Göttingen will continue to support these programs to promote international exchange at all levels and for further interaction with our partners worldwide.

Prof. Dr. Ulrike Beisiegel

(President of the Georg-August University of Göttingen)

Letter from the Max Planck Society

The mission of the Max Planck Society is to conduct basic research in science and humanities at the highest level. More than 80 Max Planck Institutes are located on scientific campuses across Germany, most of them close to universities.

Scientific ties between Max Planck Institutes and universities are traditionally strong. In 1998, during the 50th year celebration of the Max Planck Society in Göttingen, the Max Planck Society, together with the Hochschulrektorenkonferenz, launched the International Max Planck Research Schools as a new joint program to further intensify cooperation.

The goals of the International Max Planck Research Schools are

- to attract excellent students from all around the world to intensive Ph.D. training programs in Germany, preparing them for careers in science,
- to integrate Max Planck scientists in top-level scientific training of junior scientists,
- to intensify the ties to the universities owing to the participation of internationally renowned Max Planck scientists in joint teaching activities, and
- to strengthen international relationships by providing individual support to each student and by exposing foreign students to German culture and the German language.

By now, 61 International Max Planck Research Schools have been established involving 71 Max Planck Institutes, 32 German universities and 26 universities abroad. About 3,050 PhD students from 120 countries are presently enrolled.

More than 3,320 PhD students have graduated to date from an International Max Planck Research School.

Since their foundation in the year 2000, the Göttingen International Max Planck Research Schools in Molecular Biology and Neuroscience have met with extraordinary success. Every year, the programs receive hundreds of applications, with the quality of the students consistently being very high. Most students graduated so far have moved on to postdoctoral positions, many at prestigious international institutions. In the past years, the Göttingen Schools received unanimous acclaim during external evaluations and won national awards. For instance they are the only Life Science Programs within Germany that were selected for the “Top Ten International Master’s Degree Courses 2006”. The Schools have also re-shaped the local scientific community, strengthening the ties between the participating institutions, and initiated new scientific collaborations that augment the international reputation of Göttingen as a center of scientific excellence. Furthermore, the Schools served as role models and founding members of the Göttingen Graduate School for Neurosciences, Biophysics, and Molecular Biosciences, thus being instrumental for the continued support by the German Excellence Initiative provided to the university. We hope that in the years to come the students of the International Max Planck Research Schools will be successful in their professional careers. We also hope that they will remember their training period in Göttingen as an exciting and stimulating phase in their lives.

Martin Stratmann
President
Max Planck Society

Marina Rodnina
Dean of the IMPRS
Molecular Biology

Overview

This yearbook is intended to provide information on the international MSc/PhD Molecular Biology Program in Göttingen, Germany, which was established in the year 2000 as a joint venture of the University of Göttingen and its non-university partners. It is also supported by the Max Planck Society as an International Max Planck Research School (IMPRS). In addition to general information on the program, the yearbook introduces the MSc students of the 2015/16 class, the faculty members, the program committee and the coordination team.

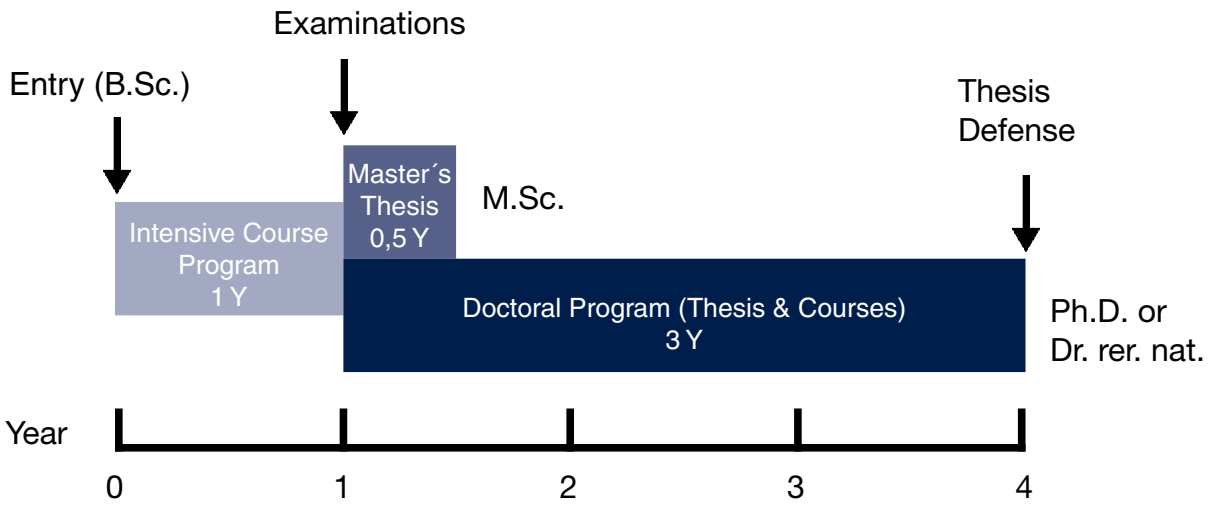
The program belongs to the Göttingen Graduate School for Neurosciences, Biophysics, and Molecular Biosciences (GGNB), which is funded by the Excellence Initiative of the German Federal and State Governments. It is offered by the Göttingen Center for Molecular Biosciences (GZMB), the Max Planck Institute for Biophysical Chemistry, the Max Planck Institute for Experimental Medicine, and the Leibniz Institute of Primate Research (German Primate Center). Further to their active participation in the Molecular Biology Program and the research activities of the GZMB, the above-mentioned partners closely cooperate in several research alliances, collaborative research centers, and interdisciplinary doctoral programs.

The intensive, research-oriented curriculum of the International MSc/PhD Molecular Biology Program qualifies students for professional work in the fields of molecular and cellular biosciences. The program is open to students from Germany and from abroad, who hold a Bachelor‘s degree (or equivalent) in the biosciences, chemistry, medicine, or related fields. Scholarships are available. All courses are held in English. The academic year starts in October and is preceded by a three-week orientation program. Applications may be submitted until January 15 of the year of enrollment. To ensure a high standard of individual training, the number of participants is limited to 20 students per year.

All students initially participate in one year of intensive course work. This first segment of the program comprises lectures, tutorials, seminars, methods courses, training in professional skills, and individually supervised research projects (laboratory rotations). The traditional German structure of academic semesters is not followed. The condensed schedule allows students to accumulate 90 credits (ECTS) within one year, which would normally require three semesters.

Subsequently, two separate segments are offered:

- **PhD Program:** Good to excellent results after the first year qualify for direct admission to a three-year doctoral project in one of the participating research groups. The Master's thesis requirement is waived in this case. After successful defense of a doctoral thesis, the degree Doctor of Philosophy (Ph.D.) or the equivalent title *Doctor rerum naturalium* (Dr. rer. nat.) is conferred.
- **MSc Program:** Alternatively, students may conclude the program with a Master's thesis, based on six months of experimental scientific research. The degree Master of Science (MSc) is awarded upon successful completion of the Master's thesis.



Intensive Course Program (First Year)

Throughout the first year, current topics in molecular biology are covered by

- lectures
- tutorials
- methods courses
- laboratory rotations
- seminars

Lectures and Tutorials

A comprehensive lecture series is offered in a sequence of 6-12 week units. The following topics are taught at an advanced level throughout the first year (36 weeks, 4 hours per week):

Module M.MolBio.11: DNA and Gene Expression

- architecture of the cell
- DNA and chromatin structure, epigenetics
- DNA replication and repair
- transcription, RNA splicing, RNA quality control
- RNA-based regulation of prokaryotes and eukaryotes
- translation, protein structures and folding, posttranslational modification
- enzyme mechanisms and regulation

Module M.MolBio.12: Metabolic and Genetic Networks

- basic metabolism, metabolic networks
- biological membranes
- photosynthesis
- signal transduction
- genomics, microbiomes

Module M.MolBio.13: Functional Organization of the Cell / Immunology / Neuroscience

- biosynthesis of organelles, nucleocytoplasmic transport
- protein sorting and processing, membrane traffic
- ubiquitin, autophagocytosis
- cytoskeleton, cell adhesion
- meiosis
- immunology, infectious diseases, principles of pathogenicity
- cell cycle, apoptosis, cancer
- neurons, synapses, synaptic transmission
- glial cells and brain vasculature
- nervous systems, sensory systems

Module M.MolBio.14: Developmental Biology / Model Systems / Biotechnology

- developmental biology
- stem cells
- fungi, *Arabidopsis*, *Drosophila*
- *C. elegans*, *Xenopus*, zebrafish, mouse
- primates, viral systems in primate research
- biotechnology (bacteria, fungi, plants, insects)

Each lecture is accompanied by a tutorial session, where students meet with a tutorial in small groups. Tutorials involve exercises, review of lecture material, and a discussion of related topics.

Methods Courses

During the first two months of the Molecular Biology Program, students participate in a series of methods courses to introduce them to principles and practical aspects of basic scientific techniques and the handling of model organisms. During the first two weeks, two 4-day projects with proteins and nucleic acids introduce various basic and advanced techniques. Weeks 3 and 4 provide an overview over various aspects of bioinformatics. Weeks 5 to 7 comprise 6 two-day experiments on a variety of different methods indicated below. In addition, students are offered a choice of two (out of four) 5-day special courses with an integrated concept of lectures and hands-on experiments as indicated below.

Introductory 4-day methods courses (week 1-2)

- proteins
- DNA

Bioinformatics courses (week 3-4)

- advanced R
- comparative sequence analysis, phylogeny, machine learning
- protein structure & bioinformatics databases
- next generation sequencing, data analysis
- advanced NGS methods
- gene ontologies & biological networks
- advanced biological networks

Introductory 2-day methods courses (week 5-7)

- analysis or protein-protein and nucleic acid-protein interaction
- chemical and enzymatic analysis of RNA structure
- light microscopy
- analysis of cellular compartments
- cell culture
- expression analysis

Special 5-day methods courses (week 7-8)

- X-ray crystallography
- (3-D-cryo) electron microscopy
- NMR spectroscopy
- mass spectrometry / proteomics

Professional Skills in Science

Additional training is offered in four separate units to prepare the students for professional scientific communication and good scientific practice:

- scientific writing and graphics
- oral presentation of scientific results
- laboratory safety
- good scientific practice

Laboratory Rotations

Starting in January, every student conducts three independent research projects (laboratory rotations) in the participating departments. Each project is individually supervised. These involve seven weeks of experimental work, followed by one week for data analysis and presentation. For each project, a report must be completed in the format of a scientific publication. The laboratory rotations must cover three different subjects.

Seminars

Seminars start in March. The class meets weekly for two hours to discuss two student presentations. The presentations are research reports based on work from the laboratory rotations.

Examinations

After the first year of intensive training, all students take one written and two oral Master's examinations. The Master's examinations explore the students' theoretical background in topics covered by lectures and tutorials. Each oral examination investigates the qualification in selected topics of the molecular life sciences.

PhD Program

Students who have passed the Master's examinations with good or excellent results qualify for direct admission to a three-year doctoral project in one of the participating research groups without being required to complete a Master's thesis first.

The PhD program emphasizes independent research on the part of the students. Doctoral students select three faculty members as their thesis advisory committee which closely monitors progress and advises students in their research project. Laboratory work is accompanied by seminars and lecture series, a wide variety of advanced methods courses, training in scientific writing and oral presentation skills, courses in intercultural communication, bioethics and research ethics, elective courses, and participation in international conferences or workshops.

Doctoral students of the program organize the international PhD student symposium "Horizons in Molecular Biology" every year with great success, attracting outstanding speakers and up to 300 participants from all over the world. The meeting was designed by the students to promote scientific exchange between young researchers from different disciplines. Since 2007, a "Career Fair for Scientists" precedes the annual Horizons meetings. The career fair offers a unique and exciting program of career presentations, CV-Check, workshops and interviews and is also organized by the Molecular Biology students.

At the end of the PhD training program, a doctoral thesis is submitted either in the traditional format, or as a collection of scientific publications in internationally recognized journals along with a general introduction and a discussion of the results. The degree of a "Ph.D." or, alternatively, "Dr. rer. nat." is awarded after the successful defense of the doctoral thesis.

Master's Program

After the first year of intensive training, students may conclude the Master's part of the program with a six-month thesis project, leading to a Master of Science degree. The thesis project involves experimental work under the supervision of faculty member of the Molecular Biology Program. Students also have the opportunity to conduct their Master's thesis project at a research institution abroad.

Orientation, Language Courses, Social Activities

A two-week orientation prior to the course program provides assistance and advice for managing day-to-day life in Germany, including arrangements for bank account, health insurance, residence permit, housing, and enrolment. Students have the opportunity to meet faculty members and visit laboratories of the participating institutions. In addition, the orientation program informs students about computing and library facilities, the city and university of Göttingen, sports facilities, and cultural events.

The orientation program also includes several course units to refresh basic knowledge in chemistry and physics and introduces the students to programming in R and basic statistics.

An intensive basic language course in German is offered in cooperation with *Lektorat Deutsch als Fremdsprache* to facilitate the first weeks in Göttingen. Additional language courses and social activities accompany the program.

Application, Selection, and Admission 2015

Applicants must hold a Bachelor's degree or equivalent in biology, biochemistry, chemistry, medicine, or related fields. Applicants who are not native speakers of English should demonstrate adequate competence of the English language by acceptable results in an internationally recognized test.

In the year 2015, the Molecular Biology Program received 709 applications from 65 countries.

Continent	Applications	Admissions
Europe (total)	**105**	**9**
Germany	20	3
other West Europe	30	2
East Europe	55	4
America (total)	**32**	**0**
North America	15	0
Central/South America	17	0
Africa (total)	**146**	**3**
North Africa	74	3
Central/South Africa	72	0
Asia (total)	**425**	**8**
Near East	91	1
Central Asia/ Far East	334	7
Australia	**1**	**0**

Students 2015 / 2016

Name		Home Country
Laura	Ahumada-Arranz	Spain
Gerald Ryan	Aquino	Philippines
Robert Lorenz	Chua	Philippines
Hadil	El Sammak	Egypt
Mahmoud Tarek	Elzayat	Egypt
Katharina	Glaser	Germany
Rashi	Goel	India
Bishoy Magdy Fekry	Hanna	Egypt
Katarina	Harasimov	Serbia
Deniz	Kaya	Germany
Miriam	Klaus	Germany
Yi-Chen	Lin	Taiwan
Yi-Tse	Liu	Taiwan
Yen-Yun	Lu	Taiwan
Valentina	Manzini	Italy
Volodymyr	Mykhailiuk	Ukraine
Sofiia	Reshetniak	Ukraine
Salma	Sohrabi-Jahromi	Iran
Kristina	Stakyte	Lithuania
Sung-Hui	Yi	Taiwan

Laura Ahumada-Arranz

Spain

Laura Ahumada-Arranz

EDUCATION

College / University

University of Salamanca

Highest Degree

Master of Science (MSc)

Major Subjects

Molecular Biology, Cellular Biology and Cell Cycle

Lab Experience

Genetic engineering and cloning in *S. cerevisiae* and *S. pombe*, PCR, site-directed mutagenesis, WB and analysis of protein PTMs, histology sample processing, immunohistochemistry and fluorescence microscopy

Projects / Research

2014 – 2015 "Control of PCNA deubiquitylation in the cell cycle of *S. cerevisiae*"

2013 – 2014 "The Evolutionary Conservation of PCNA Phosphorylation at Y211 in the Replication of *S. cerevisiae* and *S. pombe*", Master's thesis

2012 – 2013 "Effect of MSCs Treatment in an Ocular Graft-vs-host Disease Model", research assistant

2013 "Cellular Therapy in the CNS in a Murine Model for Selective Neuronal Death", internship

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

2012 – 2013 Spanish Ministry of Education Scholarship for a research fellowship

2012 Award from the University of Salamanca for an undergraduate internship

2011 German language course at Ruprecht-Karls-Universität Heidelberg

Gerald Ryan Aquino

Philippines

Gerald Ryan Aquino

EDUCATION

College / University

University of the Philippines-Diliman

Highest Degree

Master of Science

Major Subjects

Molecular Biology and Biotechnology

Lab Experience

DNA and RNA extraction, conventional and real-time PCR, agarose and polyacrylamide gel electrophoresis, molecular cloning, animal and bacterial cell culture, basic microbiology techniques, ELISA, basic microscopy and flow cytometry, zebrafish breeding and maintenance

Projects / Research

2012 – 2015 "Design and Optimization of a Padlock Probe Platform to Genotype Single Nucleotide Polymorphisms Associated with Clopidogrel Resistance"

2013 – 2015 "Detection of *Plasmodium falciparum* and *P. vivax* using 18S rRNA Gene Sub unit-Based Real-Time PCR"

2010 – 2012 "Single Nucleotide Polymorphism Genotyping of Anti-Thrombotic Therapy Resistance Markers Using Tetra-Primer Arms PCR and High Resolution Melting Analysis"

2009 – 2010 "Cu/Zn Superoxide Dismutase Gene is Transcriptionally Up-regulated in the Liver of Zebrafish (*Danio rerio*) Following Acute Exposure to Hexavalent Chromium"

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

Philippines

Robert Lorenz Chua

EDUCATION

College / University

University of the Philippines-Diliman

Highest Degree

Bachelor of Science

Major Subjects

Molecular Biology and Biotechnology

Lab Experience

Various techniques in molecular and cellular biology including PCR, semi-quantitative RT-PCR, site-directed mutagenesis via gene SOEing, DNA, RNA and protein extraction, molecular cloning, western blot, light and fluorescence microscopy, transient transfection of mammalian cells, cytochemistry, luciferase assays, MTS assays, and scratch-wound healing assays

Projects / Research

6/2014 – 9/2015 “Functional sequelae of CRNDE overexpression”

6/2014 – 9/2015 “Regulation of S100P methylation by putative competitive endogenous RNAs: S100PBP and TET3”

11/2014 – 9/2015 “Preliminary investigations on the regulation of CYP3A4 by microRNAs and mirSNPs”

4/2012 – 9/2015 “Expression of drug-metabolizing enzyme, CYP1A2, is subject to microRNA regulation

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

Egypt

Hadil El Sammak

EDUCATION

College / University

German University in Cairo (GUC)

Highest Degree

Bachelor of Science (B.Sc.)

Major Subjects

Pharmaceutical Science and Biotechnology

Lab Experience

Molecular Biology techniques as nucleic acid extraction, PCR, gel electrophoresis, DNA sequencing and cell culture techniques, in addition to Analytical techniques as chromatography and spectroscopy

Projects / Research

2014 Testing the activity of chalcones derivatives and detecting their mechanism of action on several mammalian cancer cell lines. (Assistant Prof. Iman Gomaa, at the Molecular and Cellular Biology Research Group, GUC, Cairo –Egypt)

2012 Degradation of xenobiotics found in water using bacterial cultures (Dr. Mohamed El Azizi, at the Microbiology Lab, GUC, Cairo- Egypt)

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

2014 DAAD Scholarship for Drug Design Summer School at the University of Tübingen

2011, 2013 GUC Academic Excellence Award

Mahmoud Tarek Elzayat

Egypt

Mahmoud Tarek Elzayat

EDUCATION

College / University

German University in Cairo

Highest Degree

Bachelor of Science

Major Subjects

Pharmaceutical Science and Biotechnology

Lab Experience

Basic molecular biology techniques including polymerase chain reaction (conventional and colony PCR), RNA extraction, DNA (plasmid) extraction, transmission of plasmid into bacterial cells and preparation of electro competent bacterial cells, in addition to, gel electrophoresis, UV spectrophotometry, thin layer chromatography and HPLC.

Projects / Research

6/2014 – 9/2014 “Investigating the effect of glycogen degradation on L-histidine production in *Corynebacterium glutamicum*.” Department of Microbiology and Biotechnology, headed by Prof. Bernhard Eikmanns. Universität Ulm, Ulm, Germany

8/2013 – 9/2013 Intern at the US. Navy Medical Research Unit 3 (NAMRU-3) in the vector biology research program (VBRP). Cairo, Egypt

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

8/2011 Academic Excellence Award given by DAAD and GUC to study German language in Ulm, Germany

Katharina Glaser

Germany

Katharina Glaser

EDUCATION

College / University

University of Göttingen

Highest Degree

Bachelor of Science

Major Subjects

Molecular Medicine

Lab Experience

Cell culture (human tumor cell lines, generation of mouse embryonic fibroblasts), flow cytometry, basic techniques in molecular biology and histology (Western and Southern blotting, RT-PCR, immunohistochemistry), microscopy

Projects / Research

03/15 – 08/15 “Investigation of functional responsiveness of murine uterine natural killer cells”, Obstetrics and Gynaecology, Cambridge, UK

10/14 – 11/14 “T-cell development”, Experimental Immunology, Göttingen

06/14 – 09/14 “Defective multiciliogenesis promotes COPD in different murine models”, Bachelor thesis, Molecular Oncology, Göttingen

01/14 – 03/14 “BRMS-1 as new target in melanoma therapy”, Molecular Oncology, Göttingen

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

2012 – present German National Academic Foundation (Studienstiftung des deutschen Volkes)

Rashi Goel

India

Rashi Goel

EDUCATION

College / University

Sri Venkateswara College, University of Delhi

Highest Degree

Bachelor of Science (Honors)

Major Subjects

Biochemistry, Molecular Biology, Cell Biology, Genetics, Immunology

Lab Experience

Animal and bacterial cell culture, DNA/RNA isolation, transformation, gel electrophoresis, ELISA, Western blotting, protein chromatography

Projects / Research

12/2014 – 8/2014 Winter School on Foundations of Ecology and Evolution at IISER, Pune

5/2014 – 7/2014 "Identification of protein components in Fragile X Mental Retardation Protein (FMRP) containing RNA induced silencing complex (RISC)" at InStem, Bangalore with Dr. Ravi Muddashetty

5/2013 – 7/2013 "A study of long non-coding RNA".Summer Internship at Jawaharlal Nehru University (JNU), New Delhi with Prof. P.C. Rath

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

2014 Stipend by Indian Academy of Sciences for Summer Research Fellowship

2012 – 2015 INSPIRE Scholarship by the Department of Science and Technology, Government of India to top 1% students in India, CBSE, Class XII Examinations

Bishoy Hanna

Egypt

Bishoy Hanna

EDUCATION

College / University

German University in Cairo (GUC)

Highest Degree

Bachelor of Science (B.Sc.) in Pharmaceutical Sciences and Biotechnology, GUC

Diploma in Microbiology and Immunology, Faculty of Pharmacy, Cairo University

Major Subjects

Pharmaceutical Sciences and Biotechnology

Lab Experience

Various techniques in biochemistry and molecular biology such as spectroscopy, chromatography, bacterial transformation, DNA and RNA isolation, PCR, protein purification and gel electrophoresis

Projects / Research

8/2011 – 10/2011 "Investigating the crystal structure of the 26S proteasomal subunits Rpn8 and Rpn11" Prof. Baumeister's lab, Max Planck Institute for Biochemistry, Martinsried, Germany

7/2010 – 8/2010 Internship in Prof. Sprenger's lab, Institute of Microbiology, Stuttgart University

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

2015 KAAD Scholarship

2008 Degree of Excellence in Physiology

2007 GUC full academic scholarship

Katarina Harasimov

Serbia

Katarina Harasimov

EDUCATION

College / University

University of Novi Sad, Department of Biology and Ecolog

Highest Degree

Bachelor of Science

Major Subjects

Molecular Biology

Lab Experience

Basic laboratory techniques in the field of molecular biology (PCR, gel electrophoresis, molecular cloning, chromatography etc.)

Projects / Research

10/2014 – 9/2015 Dormancy Base project— The main goal of this project was to build a comprehensive database of gene and protein expression during the dormant stage of a variety of animals, with a special focus on Class Insecta. Project under supervision of PhD Zeljko Popovic, Laboratory for Biochemistry, Department of Biology and Ecology, University of Novi Sad

Scholarships / Awards

2015 – 2016 DAAD Study Scholarship for Graduate Studies

2013 – 2015 Scholarship of the Foundation for Awarding and Encouraging Progress of Gifted Students, Young Scientists and Artists of the University of Novi Sad

2012 – 2013 Student Scholarship of the Ministry of Education, Science and Technological Development of the Republic of Serbia

Deniz Kaya

Germany

Deniz Kaya

EDUCATION

College / University

University of Göttingen

Highest Degree

Bachelor of Science in Molecular Biosciences

Major Subjects

Biochemistry, Developmental and Cell Biology, Microbiology, Cell and Molecular Biology of Plants, Genetics and Microbial Biology, Anthropology

Lab Experience

PCR, gel electrophoresis, immunohistochemistry, qRT-PCR, confocal microscopy, SDS-PAGE, Western Blot, spectrophotometry, cell culture, basics in bioinformatics analysis using R, X-Gal / MUG assay, gram staining

Projects / Research

3/2015 – 7/2015 Bachelor thesis project in the lab of Prof. Mansouri at the MPI for Biophysical Chemistry in Göttingen

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

Germany

Miriam Klaus

EDUCATION

College / University

Freie Universität Berlin

Highest Degree

Bachelor of Science

Major Subjects

Biochemistry

Lab Experience

Standard laboratory techniques such as protein purification and nucleic acid isolation; methods to evaluate molecule interactions including ITC, EMSA, fluorescence polarization and phage display as well as basic cell culture work coupled with gene expression assays

Projects / Research

3/2015 – 6/2015 “Examining the interaction of FBP21 and its potential binding partners”; Research group ‘Freund’, Freie Universität Berlin, Germany

8/2014 – 1/2015 “Inhibiting the SOX18 transcription factor with oligonucleotide decoys”; Research group ‘Jauch’, Guangzhou Institutes of Biomedicine & Health, Guangzhou, PR China

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

2014 German Academic Exchange Service (DAAD) RISE Stipend

2014 German Academic Exchange Service (DAAD) PROMOS Stipend

Taiwan

Yi-Chen Lin

EDUCATION

College / University

University of Copenhagen, Denmark (9/2014 – 6/2015)

National Taiwan University, Taiwan (9/2010 – 8/2014)

Highest Degree

Bachelor of Science in Agriculture with a minor in Life Science

Major Subjects

Forestry and Life Science

Lab Experience

Summer research intern, Lab of light-mediated gene expression and signal transduction in *Arabidopsis*, Institute of Plant and Microbial Biology, Academia Sinica, Taiwan

Projects / Research

7/2012 – 9/2012 Screening of Transgenic *Arabidopsis* Carrying Site-Specific Mutations in *AtbZIP16* Gene, Institute of Plant and Microbial Biology, Academia Sinica, Taiwan

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

2014 – 2015 Scholarships for excellent student to study abroad, Ministry of Education Taiwan

2013 – 2014 Presidential Award, Department of Forestry and Resource Conservation, National Taiwan University

2012 Scholarships of Chinese Forestry Association

Taiwan

Yi-Tse Liu

EDUCATION

College / University

National Taiwan University

Highest Degree

Master of Science

Major Subjects

Biochemical Science and Technology

Lab Experience

Molecular cloning and genetic engineering; recombinant protein expression and purification; protein-protein interaction assays; plant and bacterial cell culture; plant hormone and metabolite extraction and purification

Projects / Research

7/2014 – 8/2014 "Analysis of primary and secondary metabolites of *Arabidopsis* and tomatoes by LC-MS and GC-MS", Intern at Dr. Alisdair Fernie's lab

9/2012 – 6/2014 "Functional Analysis of Transcription Factor NAC13 Involved in Hairy Root Formation in *Arabidopsis*", Master's thesis, Prof. Dr. Kung-Ta Lee's lab

11/2010 – 6/2012 "Metabolomic changes of rol gene deficient *Nicotiana tobaccum* hairy roots", Bachelor's thesis, Prof. Dr. Kung-Ta Lee's lab

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

2014 Scholar of the 14th MOST-DAAD Summer Institute Program

2014 Dean Award, College of Life Science, National Taiwan University

2011 College Student Research Scholarship, Taiwan National Science Council

Taiwan

Yen-Yun Lu

EDUCATION

College / University

National Taiwan University

Highest Degree

Bachelor of Science

Major Subjects

Biochemical Science and Technology

Lab Experience

Undergraduate researcher, Laboratory of Cell Biology, National Taiwan University, Department of Biochemical Science and Technology (2013-2014)

Projects / Research

The ubiquitylation of Cten protein in human cells

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

2014 Dean Award, College of Life Science, National Taiwan University

2014 Selected as an honorary member of The Phi Tau Phi Scholastic Honor Society of The Republic of China

2013 Outstanding Student Scholarship of NTU Alumni Association

Italy

Valentina Manzini

EDUCATION

College / University

University of Sussex, England

Highest Degree

Bachelor of Science (Honors) in Biomedical Science

Major Subjects

Genetics and Genomics, Cell Biology, Gene Expression, Microbiology, Clinical Biochemistry, Cell Signalling

Lab Experience

Molecular biology techniques including plasmid preparation, random and site-directed mutagenesis, subcloning, restriction digests, DNA sequencing, PCR, western/southern blotting, trichloroacetic acid protein precipitation, chromatin immunoprecipitation. Yeast techniques with both *S.cerevisiae* and *S. pombe* including transformation, yeast genomic DNA preparation, plasmid rescue, yeast two-hybrid,spot test assay and gap-repair

Projects / Research

6/2014 – 9/2014 “Mechanism and evolutionary conservation of the interaction between SUMO and telomeric protein Stn1”. JRA summer project, University of Sussex

9/2014 – 1/2015 “Regulation of telomerase at fission yeast telomeres”. Bachelor’s thesis, University of Sussex

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

2014 Junior Research Associate (JRA) Bursary by the University of Sussex

Ukraine

Volodymyr Mykhailiuk

EDUCATION

College / University

Taras Shevchenko National University of Kyiv

Highest Degree

Bachelor of Science (B.Sc.)

Major Subjects

Biology (Minor: Biochemistry)

Lab Experience

Topoisomerase I *in vitro* assay, protein and DNA PAG electrophoresis, DNA extraction, isolation, restriction, agarose gel electrophoresis, Fluorescent Intercalator Displacement assay, binding constant evaluation, spectrophotometry, Telomeric Repeat Amplification Protocol assay, bacterial cell transformation

Projects / Research

1/2012 – 9/2015 “Influence of novel acridine derivatives on topoisomerase I activity in *in vitro* relaxation system.” / “Fluorescent labeling of proteins with novel dioxaborine dyes.” Institute of Molecular Biology and Genetics, National Academy of Sciences of Ukraine, Kyiv, Ukraine

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

2011 – 2014 Ukrainian governmental enhanced scholarship for academic excellence

Sofiia Reshetniak

Ukraine

Sofiia Reshetniak

EDUCATION

College / University

Taras Shevchenko National University of Kyiv

Highest Degree

Bachelor of Science (B.Sc.)

Major Subjects

Biology (Minor: Molecular Biology)

Lab Experience

Work with mammalian and bacterial cell cultures, subcellular fractionation of mammalian cells and tissues, agarose and polyacrylamide gel electrophoresis, Western blot analysis, immunofluorescence cell staining, protein complexes co-immunoprecipitation, PCR, molecular cloning assays, light and fluorescent microscopy

Projects / Research

5/2012 – 2/2015 Studies of cellular localization and it's regulation of intersectin 1. Institute of Molecular Biology and Genetics, National Academy of Sciences of Ukraine, Kyiv, Ukraine

Scholarships / Awards

2015 – 2016 DAAD scholarship for graduates of all disciplines

2010, 2011, 2012, 2015 The Increased Excellence Stipend of Taras Shevchenko National University of Kyiv

Salma Sohrabi-Jahromi

Iran

Salma Sohrabi-Jahromi

EDUCATION

College / University

University of Tehran

Highest Degree

Master of Science

Major Subjects

Molecular Biotechnology

Lab Experience

Familiar with C++ and Matlab programming, mathematical modelling, statistical analysis, analysing transcriptomic and proteomic data, standard molecular biology techniques like cell culture, PCR, cloning, gel electrophoresis, chromatography, blotting, mutagenesis, and routine microbial techniques

Projects / Research

2014 – 2015 "Introducing a kidney-specific genome-scale metabolic network model for analyzing focal segmental glomerulosclerosis (FSGS)." Department of Biotechnology, University of Tehran

2014 "Designing novel inhibitors for Thrombin-activatable fibrinolysis inhibitor." Faculty of Pharmacy, Tehran University of Medical Sciences

2013 – 2014 "Studying the distribution of important reactions in *E. coli* metabolic network." Department of Biotechnology, University of Tehran

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

2010 – 2015 Iran's National Elites Foundation scholarship

2010 – 2015 University of Tehran Fellowship for Exceptional Talents

Lithuania

Kristina Stakyte

EDUCATION

College / University

The University of Edinburgh

Highest Degree

Bachelor of Science with Honors in Biological Sciences (Biochemistry)

Major Subjects

Biochemical techniques, structural biology, structures and functions of proteins, membrane biology, molecular cell biology, molecular genetics

Lab Experience

Basic biochemical, molecular and cell biology techniques

Projects / Research

5/2015 – 8/2015 Expression and purification of Rax1 and Rax2 (WTCCB)

1/2015 – 5/2015 Regulation of Mto2 homodimerization by cell cycle-dependent phosphorylation (WTCCB)

5/2014 – 8/2015 Nuclear-specific Hsp90 inhibition (MPI-IE)

6/2013 – 8/2013 Methylation status of genes during differentiation process in blood cancer cells (VU Institute of Biochemistry)

5/2013 – 6/2013 Reptin purification and drug-induced oligomerization (ECRC)

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

2015 – Scholarship by The University of Edinburgh

2014 – DAAD Research Internships in Science and Engineering scholarship

2013 – Scholarship by the Research Council of Lithuania

Taiwan

Sung-Hui Yi

EDUCATION

College / University

National Taiwan University

Highest Degree

Master of Science

Major Subjects

Biochemical Science and Technology

Lab Experience

My master's thesis was specified on protein-protein interactions analysis. I used yeast two-hybrid and bimolecular fluorescence complementation as the main tool. Some other experiments from analyzing biological molecules to culturing different genetic-modified organisms were also used

Projects / Research

2014 (summer) Intern project: "Analysis of gene expressions and morphologies in AM fungi infected root systems". Prof. Dr. Franziska Krajinski's group, Max Planck Institute of Molecular Plant Physiology, Potsdam, Germany

2012 – 2014 Master's thesis: "Interactomic Study of Root Locus B in Tobacco Hairy Roots". Prof. Kung-Ta Lee's group, Department of Biochemical Science and Technology, National Taiwan University, Taipei, Taiwan

Scholarships / Awards

2015 – 2016 Stipend by the International Max Planck Research School

2014 14th DAAD/MOST Summer Institute Program

2014 Dean's Award of College of Life Science, National Taiwan University

2011 – 2012 Presidential Awards of National Taiwan University

Faculty

Name		Group / Institution	
Mathias	Bähr	Neurology	U Göttingen
Holger	Bastians	Cellular Oncology	U Göttingen
Tim	Beißbarth	Statistical Bioinformatics	U Göttingen
Markus	Bohnsack	Molecular Biology	U Göttingen
Gerhard H.	Braus	Molecular Microbiology and Genetics	U Göttingen
Bertram	Brenig	Molecular Biology of Livestock	U Göttingen
Henrik	Bringmann	Sleep and Waking	MPI bpc
Nils	Brose	Molecular Neurobiology	MPI em
Patrick	Cramer	Molecular Biology	MPI bpc
Rolf	Daniel	Genomic and Applied Microbiology	U Göttingen
Matthias	Dobbelstein	Molecular Oncology	U Göttingen
Roland	Dosch	Molecular Control of Zebrafish Oogenesis	U Göttingen
Jörg	Enderlein	Biophysics	U Göttingen
Ivo	Feußner	Plant Biochemistry	U Göttingen
Ralf	Ficner	Molecular Structural Biology	U Göttingen
Wolfgang	Fischle	Chromatin Biochemistry	MPI bpc
Christiane	Gatz	Plant Molecular Biology and Physiology	U Göttingen
Dirk	Görlich	Cellular Logistics	MPI bpc
Christian	Griesinger	NMR-based Structural Biology	MPI bpc
Uwe	Groß	Medical Microbiology	U Göttingen
Jörg	Großhans	Developmental Biochemistry	U Göttingen
Helmut	Grubmüller	Theoretical and Computational Biophysics	MPI bpc
Heidi	Hahn	Human Genetics	U Göttingen
Kai	Heimel	Microbial Cell Biology	U Göttingen
Stefan	Hell	NanoBiophotonics	MPI bpc
Claudia	Höbartner	Nucleic Acid Chemistry	MPI bpc
Herbert	Jäckle	Molecular Developmental Biology	MPI bpc
Reinhard	Jahn	Neurobiology	MPI bpc
Stefan	Jakobs	High Resolution Microscopy in Neurodegenerative Diseases	MPI bpc
Andreas	Janshoff	Biophysical Chemistry	U Göttingen
Steven	Johnsen	Translational Cancer Research	U Göttingen
Michael	Kessel	Developmental Biology	MPI bpc
Dieter	Klopfenstein	Kinesin Motor-Cargo Interactions and Membrane Transport	U Göttingen
Wilfried	Kramer	Molecular Genetics	U Göttingen
Heike	Krebber	Molecular Genetics	U Göttingen
Volker	Lipka	Plant Cell Biology	U Göttingen
Reinhard	Lührmann	Cellular Biochemistry	MPI bpc
Ahmed	Mansouri	Molecular Developmental Genetics	MPI bpc
Burkhard	Morgenstern	Bioinformatics	U Göttingen
Tobias	Moser	Auditory Neuroscience	U Göttingen
Klaus-Armin	Nave	Neurogenetics	MPI em
Vladimir	Pena	X-Ray Crystallography	MPI bpc
Tomas	Pieler	Developmental Biochemistry	U Göttingen
Stefanie	Pöggeler	Genetics of Eukaryotic Organisms	U Göttingen
Stefan	Pöhlmann	Infection Biology	DPZ
Peter	Rehling	Biochemistry	U Göttingen
Silvio	Rizzoli	Neuro- and Sensory Physiology	U Göttingen
Marina	Rodnina	Physical Biochemistry	MPI bpc
Melina	Schuh	Meiosis	MPI bpc
Reinhard	Schuh	Molecular Organogenesis	MPI bpc
Blanche	Schwappach	Molecular Biology	U Göttingen
Halyna	Shcherbata	Gene Expression and Signaling	MPI bpc
Holger	Stark	Structural Dynamics	MPI bpc
Claudia	Steinem	Biomolecular Chemistry	U Göttingen
Jörg	Stülke	General Microbiology	U Göttingen
Michael	Thumm	Molecular Cell Biology	U Göttingen
Kai	Tittmann	Molecular Enzymology	U Göttingen
Henning	Urlaub	Bioanalytical Mass Spectrometry	MPI bpc
Lutz	Walter	Primate Genetics	DPZ
Jürgen	Wienands	Cellular and Molecular Immunology	U Göttingen
Ernst	Wimmer	Developmental Biology	U Göttingen

U Göttingen = Georg August University, MPI bpc = Max Planck Institute for Biophysical Chemistry, MPI em = Max Planck Institute for Experimental Medicine, DPZ = German Primate Center

Address

Department of Neurology
University Medical Center
Göttingen
Robert-Koch-Str. 40

37075 Göttingen
Germany

phone: + 49-551-39 66603
fax: + 49-551-39 9348
e-mail: mbaehr@gwdg.de

Further Information

http://www.baehrlab.med.uni-goettingen.de/

Mathias Bähr

Professor of Neurology

- 1985 MD, University of Tübingen Medical School, Training in Neurology at University Hospitals in Tübingen and Düsseldorf
- DFG and Max Planck Fellow at the Max Planck Institute for Developmental Biology Tübingen and at the Department of Anatomy and Cell Biology, Washington University St.Louis
- Schilling-Foundation Professor for Clinical and Experimental Neurology, University of Tübingen
- Director at the Department of Neurology, University of Göttingen since 2001

Major Research Interests

Neuronal cell loss is not only a major feature of human neurodegenerative diseases like Parkinson's disease (PD), Alzheimer's disease (AD) or stroke, but can also be observed in neuroinflammatory conditions like Multiple Sclerosis (MS) or after traumatic lesions, e.g. of the optic nerve. We examine the cellular and molecular mechanisms of neuronal dysfunction and neuronal cell death in animal models of the respective disorders with the ultimate goal to detect new targets for a therapeutic neuroprotective intervention.
We have used for many years the retino-tectal system in rodents as our standard model to study de-and regeneration *in vitro* and *in vivo*. Our group has in detail analysed the cellular and molecular cascades that follow lesions of the optic nerve and ultimately lead to cell death of the retinal ganglion cells. To monitor the changes that occur directly after lesions we succeeded in implementing *in vivo* life-imaging of the rat and mouse optic nerve, which offers us a unique opportunity to study the complex processes that follow traumatic or inflammatory lesions of CNS fibre tracts.
In classical neurodegeneration research we have choosen PD as our topic. In this field, a multidisciplinary research team with our participation in the area C2 of the excellence cluster CNMPB examines the role of a-synuclein aggregation for dopaminergic dysfunction and cell death and characterizes other disease related proteins in order to develop new neuroprotective strategies.
In all our model systems we use AAV-mediated viral gene transfer to express different disease-or de-/regeneration associated genes as research tools and also as potential therapeutic factors to manipulate the respective molecular events *in vitro* and *in vivo*. To that end, we have e.g. developed regulatory elements that allow a controlled gene expression in complex *in vivo* models.
The final aim of our research approaches is to describe in detail the molecular pathophysiology that leads to axonal and neuronal loss and to develop new therapeutic strategies, some of which have already been translated into proof of concept studies in human patients.

Selected Recent Publications

Knöferle J, Koch JC, Ostendorf T, Michel U, Planchamp V, Vutova P, Tönges L, Stadelmann C, Brück W, Bähr M, Lingor P (2010) Mechanisms of acute axonal degeneration in the optic nerve *in vivo*. Proc Natl Acad Sci U S A 107(13): 6064-9

Koch JC, Knöferle J, Tönges L, Michel U, Bähr M, Lingor P (2011) Imaging of rat optic nerve axons *in vivo*. Nat Protoc. 3;6(12): 1887-96

Doeppner TR, Kaltwasser B, Fengyan J, Hermann DM, Bähr M (2013) TAT-Hsp70 induces neuroprotection against stroke via anti-inflammatory actions providing appropriate cellular microenvironment for transplantation of neural precursor cells. J Cereb Blood Flow Metab. 33(11): 1778-88

Kretzschmar B, Hein K, Moinfar Z, Könnecke B, Sättler MB, Hess H, Weissert R, Bähr M (2014) Treatment with atacicept enhances neuronal cell death in a rat model of optic neuritis. J Neuroimmunol. Mar 15;268(1-2): 58-63

Eckermann K, Kügler S, Bähr M (2015) Dimerization propensities of Synucleins are not predictive for Synuclein aggregation. Biochim Biophys Acta 1852(8): 1658-64

Ribas VT, Schnepf B, Challagundla M, Koch JC, Bähr M, Lingor P (2015) Early and sustained activation of autophagy in degenerating axons after spinal cord injury. Brain Pathol. 25(2): 157-70

Tereshchenko J, Maddalena A, Bähr M, Kügler S (2014) Pharmacologically controlled, discontinuous GDNF gene therapy restores motor function in a rat model of Parkinson's disease. Neurobiol Dis 65: 35-42

Address

Institute for Molecular Oncology
University Medical Center Göttingen
Grisebachstr. 8

37077 Göttingen
Germany

phone: + 49-551-39 33823
fax: + 49-551-39 9320
e-mail: holger.bastians@uni-goettingen.de

Further Information

http://www.moloncol.med.uni-goettingen.de/content/researchgroups/101.html

Holger Bastians

Professor of Cellular Oncology

- Professor of Cellular Oncology, University Medical Center, Göttingen (UMG), since 2013
- Heisenberg-Professor of Cellular Oncology, University Medical Center Göttingen (UMG), 2011 – 2013
- Heisenberg fellow, Philipps-University Marburg, 2008 – 2011
- Group leader, Institute for Molecular Biology and Tumor Research (IMT), Philipps-University Marburg, 2000 – 2010
- Postdoctoral fellow with Prof. Joan Ruderman, Harvard Medical School, Boston, USA, 1996 – 1999
- Dr. rer. nat., German Cancer Research Center (DKFZ), Heidelberg, 1996

Major Research Interests

Mitosis represents the key event during the eukaryotic cell cycle during which the DNA is equally distributed onto the two daughter cells. Defects in mitotic signaling pathways are often detected in human cancer and are directly associated with the missegregation of sister chromatids resulting in chromosomal instability (CIN) and aneuploidy. In fact, this is directly linked to tumorigenesis and represents a major characteristic of human cancer. However, the molecular mechanisms underlying CIN and the genetic lesions causing aneuploidy in human cancer are largely unknown.
In addition to its fundamental role for the maintenance of chromosomal stability, mitosis represents an important target for anti-cancer therapy and many anti-mitotic drugs including taxanes and Vinca alkaloids are frequently used in the clinic to treat various malignancies. However, it is still unclear how the interference with the mitotic progression is linked to tumor cell death, the desired outcome of therapy. A knowledge of this cross-talk is required for the development of future therapy concepts.
Based on these key points of cancer research our lab is focusing on the following main questions:
1. What are the molecular mechanisms of chromosome segregation during mitosis and what are genetic lesions in human cancer responsible for chromosomal instability?
2. What are the molecular mechanisms of mitosis associated cell death after chemotherapeutic treatment and waht are the routes of chemotherapy resistance in human cancer?
3. Based on our investigations of mitotic signaling pathways we are aiming to identify novel mitotic drug targets in order to improve current therapies and to develop novel therapeutic concepts.

Selected Recent Publications

Lüddecke S, Ertych N, Stenzinger A, Weichert W, Beissbarth T, Dyczkowski J, Gaedcke J, Valerius O, Braus GH, Kschischo M, Bastians H (2015) The putative oncogene CEP72 inhibits the mitotic function of BRCA1 and induces chromosomal instability. Oncogene, in press

Stolz A, Neufeld K, Ertych N Bastians H (2015). Wnt mediated protein stabilization ensures proper mitotic microtubule assembly and chromosomal stability. EMBO Reports: 16: 490-499

Ertych N, Stolz A, Stenzinger A, Weichert W, Kaulfuß S, Burfeind P, Aigner A, Wordeman L, Bastians H (2014) Increased microtubule assembly rates influence chromosomal instability in colorectal cancer cells. Nature Cell Biol 16: 779-91

Stolz A, Ertych N, Kienitz A, Vogel C, Schneider V, Fritz B, Jacob R, Dittmar G, Weichert W, Petersen I Bastians H (2010) The CHK2-BRCA1 tumor suppressor pathway ensures chromosomal stability in human somatic cells. Nature Cell Biol 12: 492-499

Kaestner P, Stolz A, Bastians H (2009) Determinants for the efficiency of anti-cancer drugs targeting either Aurora-A or Aurora-B kinases. Mol Cancer Ther 8: 2046-2056

Stolz A, Vogel C, Schneider V, Ertych N, Kienitz A, Yu H, Bastians H (2009) Pharmacologic abrogation of the mitotic spindle checkpoint by an indolocarbazole discovered by cellular screening efficiently kills cancer cells. Cancer Research 69: 3874-3883

Address

Dept. of Medical Statistics
University Medical Center
Göttingen
Humboldtallee 32

37073 Göttingen
Germany

phone: + 49-551-39 14099
fax: + 49-551-39 4995
e-mail: tim.beissbarth@
med.uni-goettingen.de

Further Information

http://www.ams.med.uni-goettingen.de/beissb.shtml

Tim Beißbarth

Associate Professor of Biostatistics

- Dr. rer. nat, University Heidelberg, 2001
- Postdoctoral fellow, Department Computational Molecular Biology, Max-Planck-Institute for molecular Genetics, Berlin, 2001 – 2002
- Postdoctoral fellow, Department Bioinformatics, WEHI, Melbourne, Australia,
  2002 – 2005
- Group Leader, Bioinformatics & Modeling, Department Molecular Genome Analysis, DKFZ, Heidelberg, 2005 – 2008
- Professor, Statistical Bioinformatics, Department Medical Statistics, University Medical Center, Göttingen, Since 2008

Major Research Interests

The Statistical Bioinformatics group of the department of Medical Statistics is developing statistical applications at methods for biomedical research. We are closely working together with other biostatisticians/bioinformaticists as well as clinical and biological researchers. The focus of the group is the development of methods and tools to analyse biomedical data and to reconstruct biological networks. These methods are implemented mostly in the statistical computing environment of R.

Selected Recent Publications

Bayerlová M, Jung K, Kramer F, Klemm F, Bleckmann A, Beißbarth T (2015) Comparative study on gene set and pathway topology-based enrichment methods. BCM Bioinformatics (Oct 16:334)

Wachter A, Beißbarth T (2015) pwOmics: an R package for pathway-based integration of time-series omics data using public database knowledge. Bioinformatics 31(18): 3072-4

von der Hyde S, Bender C, Henjes F, Sonntag J, Korf U, Beißbarth T (2014) Boolean ErbB network reconstructions and perturbation simulations reveal individual drug response in different breast cancer cell lines. BMC Systems Biology, 8: 75

Jung K, Dihazi H, Bibi A, Dihazi GH, Beißbarth T (2014) Adaption of the global test idea to proteomics data with missing values. Bioinformatics 30(10): 1424-30

Kramer F, Bayerlová M, Klemm F, Bleckmann A, Beißbarth T (2013) rBiopaxParser - an R package to parse, modify and visualize BioPAX data. Bioinformatics 29(4): 520-2

Gade S, Porzelius C, Fälth M, Brase JC, Wuttig D, Kuner R, Binder H, Sültmann H, Beißbarth T (2011) Graph based fusion of miRNA and mRNA expression data improves clinical coutcome prediction in prostate cancer. BMC Bioinformatics 12(1): 488

Bender C, Heyde S, Henjes F, Wiemann S, Korf U, Beißbarth T (2011) Inferring signalling networks from longitudinal data using sampling based approaches in the R-package 'ddepn'. BMC Bioinformatics 2011, 12: 291

Johannes M, Fröhlich H, Sültmann H, Beißbarth T (2011) pathClass: an R-package for integration of pathway knowledge into support vector machines for biomarker discovery. Bioinformatics, 2011, 27(10): 1442-3

Jung K, Becker B, Brunner B, Beißbarth T (2011) Comparison of Global Tests for Functional Gene Sets in Two-Group Designs and Selection of Potentially Effect-causing Genes. Bioinformatics, 2011, 27(10): 1377-83

Address

Dept. of Molecular Biology
University Medical Center
Göttingen
Humboldtallee 23

37073 Göttingen
Germany

phone: + 49-551-39 5968
fax: + 49-551-39 5960
e-mail: markus.bohnsack@med.uni-goettingen.de

Further Information

http://www.uni-bc.gwdg.de/index.php?id=671

Markus Bohnsack

Professor of Molecular Biology

- Dr. rer. nat. (PhD) at the Centre for Molecular Biology Heidelberg (ZMBH), University of Heidelberg (2005)
- Postdoctoral fellow at the University of Edinburgh, UK (2006 – 2008)
- Group leader at the Goethe University, Frankfurt (2008 – 2012)
- Adjunct Investigator at the Cluster of Excellence Frankfurt (2009 – 2012)
- Professor of Molecular Biology, University Medical Centre (UMG), Göttingen (since 2012)

Major Research Interests

RNA-protein complexes play central roles in many cellular processes, including the regulation of gene expression, translation and chromatin remodelling. Our group is interested in the biogenesis, functions and dynamics of RNA-protein complexes. In particular, we focus on understanding the regulatory role they often play during development, disease and differentiation. A major research theme of the laboratory is ribosome biogenesis, a fundamental process that is required for the production of all proteins and is closely coupled to the cellular growth rate. This highly complex processes involves the co-ordinated action of multiple cofactors proteins and large number of small nucleolar RNAs (snoRNAs), which basepair with and modify the ribosomal RNA. Much of our current knowledge of this complex process is derived from studies in the yeast *Saccharomyces cerevisiae*, where more than 200 cofactors have been identified. Despite the many links between ribosome production and disease, studies into ribosome production in human cells are still in their infancy.
Multiple genetic diseases are caused by mutations in ribosome biogenesis cofactors or ribosomal proteins leading to impaired ribosome production. These diseases, termed ribosomopathies, include Bowen-Conradi syndrome, Treacher Collins syndrome and various haematological disorders. For the Bowen-Conradi syndrome, we have shown that the methyltransferase EMG1 is mis-localised from the nucleolus when it carries the disease mutation, indicating that this mutation changes the interactions of EMG1 with other cofactors. Within the group, a number of projects focus on understanding the molecular mechanisms underlying several such diseases. Other projects in the laboratory concentrate on elucidating the functions of RNA helicases in modulating the structure and dynamics of RNA-protein complexes. In ribosome biogenesis, RNA helicases are proposed to mediate essential structural remodelling of pre-ribosomal complexes and we have shown that helicases also play a critical role in the release of specific snoRNAs from pre-ribosomes. We are successfully using the UV crosslinking and analysis of cDNA (CRAC) method to identify the interaction sites of RNA helicases and other RNA-binding proteins on cellular RNAs. This allows both biochemical characterization and functional analysis of these interactions, enabling us to also understand the regulation of the activity of the proteins. Interestingly, we have recently found that many RNA helicases function in several different cellular processes, indicating that they may be important for cross-regulation of these pathways in RNA metabolism.

Selected Recent Publications

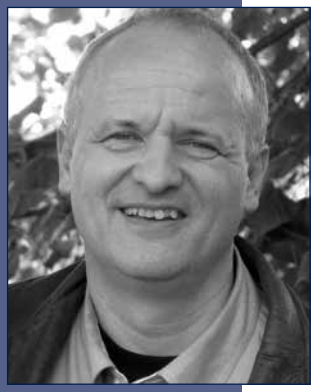
Sloan KE, Leisegang MS, Döbele C, Ramirez AS, Simm S, Safferthal C, Schorge T, Markoutsa S, Kretschmer J, Haag S, Karas M, Ebersberger I, Schleiff E, Watkins NJ, Bohnsack MT (2015) The association of late-acting snoRNPs with human pre-ribosomal complexes requires the RNA helicase DDX21. Nucleic Acids Res 43: 553-564

Haag S, Warda A, Kretschmer J, Günnigmann MA, Höbartner C, Bohnsack MT (2015) NSUN6 is a human RNA methyltransferase that catalyses formation of m5C72 in specific tRNAs. RNA 21: 1532-1543

Sloan KE, Bohnsack MT, Watkins NJ (2013) The 5S RNP couples p53 homeostasis to ribosome biogenesis and nucleolar stress. Cell Reports 5: 237-247

Meyer B, Wurm JP, Kötter P, Leisegang MS, Schilling V, Buchhaupt M, Held M, Bahr U, Karas M, Heckel A, Bohnsack MT, Wöhnert J, Entian KD (2011) The protein mutated in Bowen-Conradi Syndrome, Nep1 (Emg1), is required for a unique modification in 18S rRNA. Nucleic Acids Res 39: 1526-1537

Bohnsack MT, Martin R, Granneman S, Ruprecht M, Schleiff E, Tollervey D (2009) Prp43 bound at different sites on the Pre-rRNA performs distinct functions in ribosome synthesis. Mol Cell 36: 583-592



Address

Department of Molecular Microbiology and Genetics
University of Göttingen
Grisebachstr. 8

37077 Göttingen
Germany

phone: +49-551-39 33771
fax: +49-551-39 33330
e-mail: gbraus@gwdg.de

Further Information

http://www.uni-goettingen.de/molmibio

Gerhard H. Braus

Professor of Microbiology and Genetics

- Diploma (Biology), Albert-Ludwig University, Freiburg i. Br. (Germany), 1983
- Dr.sc.nat., Swiss Federal Institute of Technology (ETH), Zürich (Switzer land), 1987
- Habilitation (Microbiology), Swiss Federal Institute of Technology (ETH), Zürich (Switzerland), 1991
- Associate Professor of Biochemistry, Friedrich Alexander University, Erlangen (Germany), 1993 – 1996
- Since 1996 Professor of Microbiology (since 2001 Professor of Microbiology and Genetics) in Göttingen

Major Research Interests

The major focus of the laboratory is on the control of developmental programs, protein turnover, pathogenicity and the interplay between development and primary and secondary metabolism. Our models are eukaryotic microorganisms (yeasts and filamentous fungi):
(i) We are interested how light coordinates fungal development with fungal secondary metabolism and toxin production.
(ii) Nedd8 is a ubiquitin-like protein which is involved in the control of protein turnover. We study the Nedd8-system including the COP9 signalosome using fungi as model systems.
(iii) We are interested in the molecular control (protein turnover and translation) of adhesion as initial step in infection and biofilm formation.
(iv) We study fungi as models for Parkinson (yeast), fungi as pathogens of immunocompromised patients (*A. fumigatus*) and as plant pathogens (*V. longisporum*).

Selected Recent Publications

Sarikaya-Bayram Ö, Bayram Ö, Feussner L, Kim JH, Kim HS, Kaever A, Feussner I, Chae KS, Han DM, Han KH, Braus GH (2014) The membrane-bound VapA-VipC-VapB methyltransferase complex guides signal transduction for epigenetic and transcriptional control of fungal development. Dev Cell 29: 1-15 [Journal Cover]

Ahmed YL, Gerke J, Park HS, Bayram Ö, Neumann P, Ni M, Dickmanns A, Kim SC, Hyuk JH Yu*, Braus GH*, Ficner R* (2013) Fungal velvet regulators contain a DNA binding domain reminiscent of NF-kB. PLoS Biol. 11: e1001750 (*corresponding authors) [Synopsis to the paper in: PLoS Biol. 11, e1001751]

Christmann M, Schmaler T, Gordon C, Huang X, Bayram Ö, Schinke J, Stumpf S, Dubiel W, Braus GH (2013). Control of multicellular development by the physically interacting deneddylases DEN1/DenA and COP9 signalosome (2013) PLoS Genet. 9: e1003275

Rachfall N, Bandau S, Ehrenreich A, Valerius O, Braus GH (2013) RACK1/Asc1p, a ribosomal node in cellular signalling. Mol Cell Proteomics 12: 87-105

Bayram Ö, Sarikaya Bayram Ö., Ahmed YL, Maruyama J, Valerius O, Rizzoli SO, Ficner R, Irniger S, Braus GH (2012) The *A. nidulans* MAPK module AnSte11-Ste50-Ste7-Fus3 controls development and secondary metabolism. PLoS Genet 8: e1002816 [Journal Cover]

Sarikaya ÖB, Bayram Ö, Valerius O, Park HS, Irniger S, Gerke J, Ni M, Han KH, Yu JH, Braus GH (2010) LaeA control of velvet family regulatory proteins for light-dependent development and fungal cell-type specificity. PLoS Genet 6: e1001226 [Journal Cover]

Bayram Ö, Krappmann S, Ni M, Bok JW, Helmstaedt K, Valerius O, Braus-Stromeyer S, Kwon NJ, Keller NP, Yu JH, Braus GH (2008) VelB/VeA/LaeA complex coordinates light signal with fungal development and secondary metabolism. Science 320: 1504-1506 [Comment to the paper in Perspectives, Science 320: 1430-1431]

Address

Institute of Veterinary Medicine
Dept. of Molecular Biology of Livestock
University of Göttingen
Burckhardtweg 2

37077 Göttingen
Germany

phone: +49-551-39 33383
or 39 33380
fax: +49-551-39 33392
e-mail: bbrenig@gwdg.de

Further Information

http://www.tieraerztliches-institut.uni-goettingen.de

Bertram Brenig

Full Professor of Molecular Biology of Livestock

- Director of the Institute of Veterinary Medicine
- Dr. med. vet., University of Munich, Munich 1987

Major Research Interests

The main interest of the laboratory is in the structural and functional analysis of mammalian genes and genomes. We are investigating the cause of different economical important genetic traits and defects in livestock and other domestic animals.

Currently we are working on the following projects

- Molecular genetics of Malvoy cataract
- Identification of the polled-locus in cattle
- Leg and feet quality in cattle
- Early embryonal death in cattle
- CNA in canine tumorigenesis

We are using whole genome association studies (WGAS) and next generation sequencing (NGS) techniques for the identification of chromosomal regions that are linked to the traits or disorders. Fine mapping, positional cloning and candidate gene analysis are used for further elucidation.

In recent years we have also focused on the analysis of circulating nucleic acids (CNA). The repertoire of CNAs in man, cattle, and dog has been determined and differences in CNA patterns are analysed regarding different diseases, e.g. canine mamma carcinoma, or performance traits, e.g. bovine early pregnancy determination.

Selected Recent Publications

Brenig B, Schutz E, Hardt M, Scheuermann P, Freick M (2015) A 20 bp Duplication in Exon 2 of the Aristaless-Like Homeobox 4 Gene (ALX4) Is the Candidate Causative Mutation for Tibial Hemimelia Syndrome in Galloway Cattle. PloS One 10: e0129208

Floren C, Wiedemann I, Brenig B, Schutz E, Beck J (2015) Species identification and quantification in meat and meat products using droplet digital PCR (ddPCR). Food Chemistry 173: 1054-1058

Hennecke S, Beck J, Bornemann-Kolatzki K, Neumann S, Murua Escobar H, Nolte I, Hammer SC, Hewicker-Trautwein M, Junginger J, Kaup FJ et al (2015) Prevalence of the Prefoldin Subunit 5 Gene Deletion in Canine Mammary Tumors. PloS One 10: e0131280

Schutz E, Brenig B (2015) Analytical and statistical consideration on the use of the ISAG-ICAR-SNP bovine panel for parentage control, using the Illumina BeadChip technology: example on the German Holstein population. GSE 47: 3

Swalve HH, Floren C, Wensch-Dorendorf M, Schopke K, Pijl R, Wimmers K, Brenig B (2014) A study based on records taken at time of hoof trimming reveals a strong association between the IQ motif-containing GTPase-activating protein 1 (IQGAP1) gene and sole hemorrhage in Holstein cattle. Journal of Dairy Science 97: 507-519

Address

Sleep and Waking Group
Max Planck Institute for
Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 1358
fax: +49-551-3899 715
e-mail: henrik.bringmann@
mpibpc.mpg.de

Further Information

http://www.mpibpc.
mpg.de/english/research/
ags/bringmann/

Henrik Bringmann

Max Planck Research Group Leader

- Max Planck Research Group Leader since 2009
- Postdoctoral fellow at the Laboratory of Molecular Biology, Cambrigde, UK
- PhD at the Max Planck Institute for Cell Biology and Genetics, Dresden

Major Research Interests

Sleep states occur in the life of every animal studied. While the function of waking is obvious, the function of sleep is unknown. Sleep has been suggested to serve a restorative function in the nervous system. Our lab is trying to understand the function and regulation of sleep by studying different model organisms. We have started our studies by looking at sleep in the larva of the nematode *Caenorhabditis elegans*, and are also working with mice.

We are combining behavioral assays with genetics and functional imaging. We recently found a single sleep-inducing neuron in *C. elegans* that is homologous to mammalian sleep neurons. This highly simplified sleep-inducing system in a tractable genetic model provides a great starting point to understand the regulation of sleep and to manipulate sleep in order to study the function of sleep.

Selected Recent Publications

Turek M, Besseling J, Bringmann H (2015) Agarose microchambers for long-term calcium imaging of *Caenorhabditis elegans*. J Vis Exp Jun 24;(100):e52742

Turek M, Lewandrowski IL, Bringmann H (2013) An AP2 transcription factor is required for a sleep-active neuron to induce sleep-like quiescence in *C. elegans*. Current Biology 23 (22): 2215-2223

Schwarz J, Lewandrowski IL, Bringmann H (2011) Reduced activity of a sensory neuron during a sleep-like state in *Caenorhabditis elegans*. Current Biology 21 (24): R983-R984

Redemann S, Schloissnig S, Ernst S, Pozniakowsky A, Ayloo S, Hyman AA, Bringmann H (2011) Codon adaptation-based control of protein expression in *C. elegans*. Nature Methods 8: 250-252

Address

Dept. of Molecular Neurobiology
Max Planck Institute for Experimental Medicine
Hermann-Rein-Str. 3

37075 Göttingen
Germany

phone: +49-551-3899 725
fax: +49-551-3899 715
e-mail: brose@em.mpg.de

Further Information

http://www.em.mpg.de/

Nils Brose

Professor, Director at the Max Planck Institute for Experimental Medicine

- Undergraduate studies in Biochemistry, Eberhard Karls University, Tübingen, Germany (1981 – 1985)
- MSc in Physiology with Marianne Fillenz, University of Oxford, Oxford, UK (1987)
- PhD in Biology with Reinhard Jahn, Ludwig Maximilians University, Munich, Germany (1990)
- Postdoctoral training with Stephen F. Heinemann (Salk Institute, La Jolla, CA, USA) and Thomas C. Südhof (University of Texas Southwestern Medical Center, Dallas, TX, USA) (1991 – 1995)
- Research Group Leader, Max Planck Institute of Experimental Medicine, Göttingen, Germany (1995 – 2001)
- Director, Department of Molecular Neurobiology, Max Planck Institute of Experimental Medicine, Göttingen, Germany (since 2001)

Major Research Interests

Research in the Department of Molecular Neurobiology focuses on the molecular mechanisms of nerve cell development and synapse formation and function in the vertebrate central nervous system. We combine biochemical, morphological, mouse genetic, behavioral, and physiological methods to elucidate the molecular basis of nerve cell differentiation, synapse formation and transmitter release processes. Our work in the field of nerve cell development focuses on the role of protein ubiqutination and SUMOylation in cell polarity formation, cell migration, and neuritogenesis. The synaptogenesis research in our group concentrates on synaptic cell adhesion proteins, their role in synapse formation, and their dysfunction in neuropsychiatric diseases. Studies on the molecular mechanisms of neurotransmitter release focus on components of the presynaptic active zone and their regulatory function in synaptic vesicle fusion.

Selected Recent Publications

Imig C, Min SW, Krinner S, Arancillo M, Rosenmund C, Südhof TC, Rhee J, Brose N*, Cooper BH* (2014) The morphological and molecular nature of synaptic vesicle priming at presynaptic active zones. Neuron 84: 416-431 (*joint corresponding authors)

Lipstein N, Sakaba T, Cooper BH, Lin K-H, Strenzke N, Ashery U, Rhee J-S, Taschenberger H, Neher E, Brose N (2013) Dynamic control of synaptic vesicle replenishment and short-term plasticity by Ca^{2+}-Calmodulin-Munc13-1 signaling. Neuron 79: 82-96

Tirard M, Hsiao H-H, Nikolov M, Urlaub H, Melchior F, Brose N (2012) *In vivo* localization and identification of SUMOylated proteins in the brain of His6-HA-SUMO1 knock-in mice. Proc Natl Acad Sci USA 109: 21122-21127

Kawabe H, Neeb A, Dimova K, Young SM Jr, Takeda M, Katsurabayashi S, Mitkovski M, Malakhova OA, Zhang D-E, Umikawa M, Kariya K, Goebbels S, Nave K-A, Rosenmund C, Jahn O, Rhee J-S, Brose N (2010) Regulation of Rap2A by the ubiquitin ligase Nedd4-1 controls neurite development in cortical neurons. Neuron 65: 358-372

Jamain S, Radyushkin K, Hammerschmidt K, Granon S, Boretius S, Varoqueaux F, Ramanantsoa N, Gallego J, Ronnenberg A, Winter D, Frahm J, Fischer J, Bourgeron T, Ehrenreich H, Brose N (2008) Reduced social interaction and ultrasonic communication in a mouse model of monogenic heritable autism. Proc Natl Acad Sci USA 105: 1710-1715

Jockusch W, Speidel D, Sigler A, Sørensen J, Varoqueaux F, Rhee J-S, Brose N (2007) CAPS-1 and CAPS-2 are essential synaptic vesicle priming proteins. Cell 131: 796-808

Address

Dept. of Molecular Biology
Max Planck Institute for
Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

e-mail: patrick.cramer@
mpibpc.mpg.de

Further Information

http://www.mpibpc.mpg.de/
cramer

Patrick Cramer

Professor, Director at the Max Planck Institute for Biophysical Chemistry

- Study of chemistry at the Universities of Stuttgart and Heidelberg, Research student at the University of Bristol (UK) and Cambridge (UK)
- 1995 Diploma in chemistry at the University of Heidelberg
- 1998 Doctorate at the University of Heidelberg/EMBL Grenoble (France)
- 1995 –1998 Predoctoral fellow in Grenoble (France)
- 1999 – 2000 postdoctoral fellow at Stanford University (USA)
- 2001 – 2003 Tenure-track professor of biochemistry at the University of Munich
- 2004 – 2014 Professor of biochemistry at the University of Munich
- 2004 – 2013 Director at the Gene Center of the University of Munich (LMU)
- Since 2014 Director of the Department for Molecular Biology at the Max Planck Institute of Biophysical Chemistry

Major Research Interests

Molecular Biology: from molecular movies to regulatory systems

Gene transcription is the first step in the expression of the genetic information and a focal point for cellular regulation. Our goal is to understand the molecular mechanisms of gene transcription and the principles of genomic regulation in eukaryotic cells. We use integrated structural biology and complementary functional studies to unravel the three-dimensional and functional architecture of large macromolecular complexes involved in transcription. We also develop functional genomics methods and computational approaches to unravel the cellular mechanisms of genomic regulation. These efforts led to a first molecular movie of transcription and provided insights into gene-regulatory cellular networks. Together, these efforts shape the emerging fields of genome biology and molecular systems biology. Our aim is to understand the functional genome as a regulatory network based on the underlying structural and molecular mechanisms.

Selected Recent Publications

Plaschka C, Larivière L, Wenzeck L, Seizl 2, Hemann M, Tegunov D, Petrotchenko EV, Borchers CH, Baumeister W, Herzog F, Villa E, Cramer P (2015) Architecture of the RNA polymerase II-Mediator core initiation complex. Nature 518(7539): 376-80

Schulz D, Schwalb B, Kiesel A, Baejen C, Torkler P, Gagneur J, Soeding J, Cramer P (2013) Transcriptome Surveillance by Selective Termination of Noncoding RNA Synthesis. Cell 155(5): 1075-87

Engel C, Sainsbury S, Cheung AC, Kostrewa D, Cramer P. (2013) RNA polymerase I structure and transcription regulation. Nature 502(7473): 650-5

Michel M, Cramer P. (2013) Transitions for regulating early transcription. Cell 153: 943-944

Sainsbury S, Niesser J and Cramer P. (2012) Structure and function of the initially transcribing RNA polymerase II–TFIIB complex. Nature 493: 437-440

Larivière L, Plaschka P, Seizl M, Wenzeck L, Kurth F, Cramer P. (2012) Structure of the mediator head module. Nature 492: 448-451

Mayer A, Heidemann M, Lidschreiber M, Schreieck A, Sun M, Hintermair C, Kremmer E, Eick D, Cramer P. (2012) CTD tyrosine phosphorylation impairs termination factor recruitment to RNA polymerase II. Science 336: 1723-1725

Address

Dept. of Genomic and Applied Microbiology
University of Göttingen
Grisebachstr. 8

37077 Göttingen
Germany

phone: +49-551-39 33827
fax: +49-551-39 12181
e-mail: rdaniel@gwdg.de

Further Information

http://appmibio.uni-goettingen.de

Rolf Daniel

- 2013 – present: Speaker “North German Center of Microbial Genomics” (Norddeutsches Zentrum für Mikrobielle Genomforschung, NZMG)
- 04/2012 – present: Managing Director of the Institute of Microbiology and Genetics, Georg August University Göttingen
- 02/2012 – present: Full Professor (W3) Genomic and Applied Microbiology, Head of the Dept. of Genomic and Applied Microbiology & Göttingen Genomics Laboratory, Georg August University Göttingen
- 2013: Norddeutscher Wissenschaftspreis (Northern German Science Award)
- 05/2008 – 01/2012: Acting Director of the Department of Genomic and Applied Microbiology and Head of the “Göttingen Genomics Laboratory”, Georg August University Göttingen
- 06/1996 – 04/2008: Group Leader, Department of Genomic and Applied Microbiology, Georg August University Göttingen
- 06/1995 – 05/1996: Research Fellow, University of California (Berkeley, USA), Institute of Molecular and Cell Biology, Head: Prof. Dr. Randy Schekman
- 05/1994 – 05/1995: Research Fellow, Georg August University Göttingen, Department of General Microbiology

Major Research Interests

Research foci are cultivation-independent nucleic acids-based metagenomics and metatranscriptomics of complex microbial assemblages and recovery of novel genes and gene products from environmental samples such as soil, sediments, ice, and biofilms. The metagenomic screenings comprised function-based as well as sequence-based approaches. This work has led, e.g., to the successful identification and characterization proteases, cellulases, oxidoreductases, dehydratases, lipases, and DNA polymerases from metagenomes. To gain insights into the genomes of the uncultivated microorganisms and to determine metabolic potential and key functions of microbial communities in the studied environments direct sequencing and annotation of metagenomic DNA and cDNA (mRNA), and comparative genomics are carried out. Other lines of research include whole-genome sequencing, transcriptomics and functional genomics of archaea, bacteria, and microbial communities. The majority of the analyzed organisms is of industrial importance or pathogenic. The group also develops novel bioinformatic tools for data analysis and visualization.

Selected Recent Publications

Gardebrecht A, Markert S, Sievert SM, Felbeck H, Thürmer A, Albrecht D, Woll-Djukic M, Brzuszkiewicz E, Fünfhaus A, Voss J, Gollnow K, Poppinga L, Liesegang H, Garcia-Gonzalez E, Genersch E, Daniel R (2014) How to kill the honey bee larva: genomic potential and virulence mechanisms of *Paenibacillus* larvae. PLOS One 9:e90914

Voget S, Wemheuer B, Brinkhoff T, Vollmers J, Dietrich S, Giebel H.-A., Beardsley C, Sardemann C, Bakenhus I, Billerbeck S, Daniel R, Simon M (2014) Adaptation of an abundant *Roseobacter* RCA organism to pelagic systems revealed by genomic and transcriptomic analyses. ISME J doi:10.1038/ismej.2014.134

Wemheuer B, Güllert S, Billerbeck S, Giebel H-A, Voget S, Simon M, Daniel R (2014) Impact of a phytoplankton bloom on the diversity of the active bacterial community in the southern North Sea as revealed by metatranscriptomic approaches. FEMS Microbiology Ecology 87: 378-389

Nacke H, Fischer C, Thürmer A, Meinicke P, Daniel R (2014) Land use type significantly affects microbial gene transcription in soil. Microbial Ecology 67: 919-930

Schneider D, Arp G, Reimer A, Reitner J,Daniel R (2013) Phylogenetic analysis of a microbialite-forming microbial mat from a hypersaline lake of the Kiritimati Atoll, Central Pacific. PLOS ONE 8:e66662

Matthias Dobbelstein

Professor of Molecular Oncology

- Dr. med., University of Munich, 1993
- Postdoctoral fellow, Princeton University, USA, 1993 – 1996
- Group leader, University of Marburg, 1997 – 2004
- Professor of Molecular Oncology, University of Southern Denmark, Odense, 2004 – 2005
- Head of the Department of Molecular Oncology, Georg-August-Universität Göttingen, since 2005

Major Research Interests

We are trying to understand the response of cancer cells to chemotherapy. In particular, we are analyzing the impaired replication of DNA and the damage response that results from injury to DNA. Our focus is on the signaling cascades driven by DNA damage, and on the activation of the tumor suppressor p53. Technologies include the use of large scale siRNA transfection, followed by automated fluorescence microscopy, and the analysis of DNA replication by incorporation of artificial nucleosides. As a disease model, we are investigating the response of colorectal cancer to therapy. On top of classical, DNA damaging chemotherapeutics, we are evaluating other broadly acting, yet non-genotoxic drug candidates, e. g. inhibitors of histone deacetylases and heat shock proteins. On long term, we are aiming at improving the response of tumor cells to chemotherapy by combining traditional and targeted therapeutic approaches.

Selected Recent Publications

Zhang X, Schulz R, Edmunds S, Krüger E, Markert E, Gaedcke J, Cormet-Boyaka E, Ghadimi M, Beissbarth T, Levine AJ, Moll UM, Dobbelstein M (2015) MicroRNA-101 Suppresses Tumor Cell Proliferation by Acting as an Endogenous Proteasome Inhibitor via Targeting the Proteasome Assembly Factor POMP Mol Cell 59(2): 243-57

Alexandrova EM, Yallowitz AR, Li D, Xu S, Schulz R, Proia DA, Lozano G, Dobbelstein M, Moll UM (2015) Improving survival by exploiting tumour dependence on stabilized mutant p53 for treatment. Nature523(7560): 352-6

Dobbelstein M, Sørensen CS (2015) Exploiting replicative stress to treat cancer. Nat Rev Drug Discov 14(6): 405-23

Dobbelstein M, Moll U (2014) Targeting tumour-supportive cellular machineries in anticancer drug development. Nat Rev Drug Discov 13(3):179-96

Köpper F, Bierwirth C, Schön M, Kunze M, Elvers I, Kranz D, Saini P, Menon M, Walter D, Sørensen CS, Gaestel M, Helleday T, Schön M P, Dobbelstein M (2013) Damage-induced DNA replication stalling relies on MAPK-activated protein kinase 2 activity. Proc Natl Acad Sci USA 110: 16856-16861

Beyer U, Moll-Rocek J, Moll UM, Dobbelstein M (2011) Endogenous retrovirus drives hitherto unknown proapoptotic p63 isoforms in the male germ line of humans and great apes. Proc Natl Acad Sci USA 108(9): 3624-9

Braun CJ, Zhang X, Savelyeva I, Wolff S, Moll UM, Schepeler T, Ørntoft TF, Andersen CL, Dobbelstein M (2008) p53-Responsive micrornas 192 and 215 are capable of inducing cell cycle arrest. Cancer Res 68(24): 10094-104

Address

Institute of Molecular Oncology
University Medical Center Göttingen
Justus-von-Liebig-Weg 11

37077 Göttingen
Germany

phone: +49-551-39 13840
fax: +49-551-39 13713
e-mail: mdobbel@uni-goettingen.de

Further Information

http://www.moloncol.med.uni-goettingen.de

Address

Dept. of Developmental Biochemistry
University Medical Center Göttingen
Justus-von-Liebig-Weg 11

37077 Göttingen
Germany

phone: +49-551-39 14607
fax: +49-551-39 14614
e-mail: roland.dosch@med.uni-goettingen.de

Further Information

http://www.uni-bc.gwdg.de/index.php?id=583

Roland Dosch

Group Leader at the Dept. of Developmental Biochemistry

- 1994 – 1999 PhD Deutsches Krebsforschungszentrum (DKFZ), Heidelberg, Germany
- 1999 – 2003 Postdoc University of Pennsylvania, Philadelphia, USA
- 2004 – 2010 Junior group leader, University of Geneva, Switzerland
- since 2010 Group leader at the Dept. of Developmental Biochemistry, Georg August University, Göttingen

Major Research Interests

A fundamental principle of biological systems is their capacity to reproduce, which is not found in other domains of science such as chemistry or physics. In multicellular organisms like humans, this unique activity is achieved by gametes, egg and sperm. To prepare for the development of a novel organism after fertilization, the oocyte shows a fascinating organization into various compartments.
The aim of our research is to understand the molecular mechanisms, which control the cellular organization of the oocyte. For our experiments, we take advantage of the zebrafish, which in recent years emerged as an outstanding vertebrate model to investigate molecular processes *in vivo*. We previously isolated a collection of mutations in key regulators, which show defects in the organization of the oocyte. We apply a combination of molecular genetics and cutting edge genomics such as next-generation-sequencing to identify the affected genes in these mutants. In the most interesting mutants, we started to characterize the molecular function of these essential genes. For this purpose, we incorporate biochemical methods with cell biological approaches e.g. imaging to explore the dynamics of protein localization *in vivo*. With these techniques, we discovered proteins controlling the assembly of RNA-granules as an example for a membrane-free compartment. Recently, we also analyzed membrane bound compartments and identified an important regulator of secretion. Our long-term goal is to understand the intricate molecular organization of the oocyte, which prepares it for fertilization and subsequent embryogenesis.

Selected Recent Publications

Dosch R, (2015) Next generation mothers: Maternal control of germline development in zebrafish. Crit Rev Biochem Mol Biol 50: 54-68

Riemer S, Bontems F, Krishnakumar P, Gömann J, Dosch R, (2015) A functional Bucky ball-GFP transgene visualizes germ plasm in living zebrafish. Gene Expr Patterns 18: 44-52

Kanagaraj P, Gautier-Stein A, Riedel D, Schomburg C, Cerda J, Vollack N, Dosch R (2014) Souffle/Spastizin controls secretory vesicle maturation during zebrafish oogenesis. PLoS Genet 10: e1004449

Bontems F, Baerlocher L, Mehenni S, Bahechar I, Farinelli L, Dosch R (2011) Efficient mutation identification in zebrafish by microarray capturing and next generation sequencing. BBRC 405(3): 373-376

Bontems F, Stein A, Marlow F, Lyautey J, Mullins MC, Dosch R (2009) Bucky ball organizes germ plasm assembly in zebrafish. Curr Biol 19 (5): 414-22

Address

III. Physical Institute
Biophysics / Complex Systems
University of Göttingen
Friedrich-Hund-Platz 1

37077 Göttingen
Germany

phone: +49-551-39 13833
fax: +49-551-39 7720
e-mail: joerg.enderlein@physik3.gwdg.de

Further Information

http://www.joerg-enderlein.de

Jörg Enderlein

Professor of Physics

- 1981 – 86 Study of Physics at Ilya-Mechnikov-University Odessa
- 1991 PhD in Physical Chemistry (Humboldt-University Berlin)
- 2000 Habilitation in Physical Chemistry (University of Regensburg)
- 1996 – 97 PostDoc at Los Alamos National Laboratory (USA)
- 1997 – 2000 Assistent Professor (C1) at University of Regensburg
- 2001 – 2006 Heisenberg Fellow of the DFG at Forschungszentrum Jülich
- 2007 – 2008 Professor for Biophysical Chemistry at Eberhard-Karls-University Tübingen
- Since 2008 Professor for Biophysics at Georg-August-University Göttingen

Major Research Interests

Single molecule fluorescence spectroscopy and imaging, protein conformational dynamics and folding

Selected Recent Publications

Karedla N, Stein SC, Hahnel D, Gregor I, Chizhik A, Enderlein J (2015) Simultaneous Measurement of the Three-Dimensional Orientation of Excitation and Emission Dipoles. Phys Rev Lett 115(17): 173002

Chizhik AI, Rother J, Gregor I, Janshoff A, Enderlein J (2014) Metal-induced energy transfer for live cell nanoscopy. Nature Photonics 8: 124-127

Schulz O, Pieper C, Clever M, Pfaff J, Ruhlandt A, Kehlenbach RH, Wouters FS, Großhans J, Bunt G, Enderlein J (2013) Resolution doubling in fluorescence microscopy with Confocal Spinning-Disk Image Scanning Microscopy. PNAS 110: 21000–21005

Chizhik AI, Gregor I, Schleifenbaum F, Müller CB, Röling C, Meixner AJ, Enderlein J (2012) Electrodynamic Coupling of Electric Dipole Emitters to a Fluctuating Mode Density within a Nanocavity. Phys Rev Lett 108: 163002

Pieper C, Enderlein J (2011) Fluorescence correlation spectroscopy as a tool for measuring the rotational diffusion of macromolecules. Chem Phys Lett 516: 1-11

Chizhik AI, Chizhik AM, Khoptyar D, Bär S, Meixner AJ, Enderlein J (2011) Probing the Radiative Transition of Single Molecules with a Tunable Microresonator. Nano Lett 11: 1700-1703

Müller CB, Enderlein J (2010) Image scanning microscopy. Phys Rev Lett 104: 198101

Berndt M, Lorenz M, Enderlein J, Diez S (2010) Axial Nanometer Distances Measured by Fluorescence Lifetime Imaging Microscopy. Nano Lett 10: 1497-1500

Dertinger T, Colyer R, Iyer G, Weiss S, Enderlein J (2009) Fast, background-free, 3D superresolution optical fluctuation imaging (SOFI). PNAS 106: 22287-22292

Chizhik A, Schleifenbaum F, Gutbrod R, Chizhik A, Khoptyar D, Meixner AJ, Enderlein J (2009) Tuning the Fluorescence Emission Spectra of a Single Molecule with a Variable Optical Sub-wavelength Metal Microcavity. Phys Rev Lett 102: 073002-6

Address

Albrecht von Haller Institute
for Plant Sciences
Dept. of Plant Biochemistry
University of Göttingen
Justus-von-Liebig-Weg 11

37077 Göttingen
Germany

phone: +49-551-39 5743
fax: +49-551-39 5749
e-mail: ifeussn@gwdg.de

Further Information

http://www.plant-biochem.uni-goettingen.de

Ivo Feußner

Professor of Biochemistry

- Diploma (Chemistry), Philipps-University, Marburg (Germany), 1990
- Dr. rer. nat., Philipps-University, Marburg (Germany), 1993
- Leader of an independent research group at the Institute for Plant Biochemistry (IPB), Halle/Saale (Germany), 1997 – 1999
- Habilitation (Biochemistry), Martin-Luther-University, Halle/Saale (Germany), 2000
- Leader of an independent research group at Institute for Plant Genetics and Crop Plant Research (IPK), Gatersleben (Germany), 2000 – 2002
- Since 2002 Professor of Biochemistry, Georg-August-University, Göttingen (Germany)
- Awards: Habilitation-Prize of the Ernst Schering Research Foundation (2001), Terry-Galliard Medal (2012)
- Fellow of the Saxonian Academy of Sciences, Leipzig, Germany (2009)
- Fellow of the Academy of Sciences, Göttingen, Germany (2013)

Major Research Interests

The group is currently studying different aspects of the lipid metabolism of plants, algae, mosses and fungi. In this context we are primarily interested in the metabolism of structural lipids and lipid-derived signal transduction processes. For this purpose, we make use of both classical techniques as analytical chemistry and biochemistry as well as of modern approaches in the area of molecular genetics, including the generation of transgenic organisms („gain-of-function“) or mutants („loss-of-function“).
Biochemistry and function of oxylipin metabolism:
We are interested in physiological functions of lipid peroxidation processes. Thus we analyze the function of specific lipoxygenases, i.e. the role of their products, so-called oxylipins (oxygenated fatty acid derivatives), as signals or defence substances during biotic and abiotic stress. Lipid peroxidation reactions are analysed in general by metabolomic approaches and more specifically by studying the biosynthesis of aldehydes (fruit aromas) and hydroxy fatty acids (plant defence). Other studies deal with the role of oxylipins in plants, mosses and algae. In addition the catalytic mechanism of lipoxygenases and related dioxygenases is analysed.
Biochemistry of the biosynthesis of structural lipids:
Even in plants a huge number of different fatty acids are found. We are interested in enzymes which introduce new functionalities (i.e. double bonds at unusual positions or conjugated double bonds) in the fatty acid backbone in order to obtain new seed oils for biotechnological, nutritional and medical purposes. Moreover we study the biochemical pathways or networks that led to an increase in the seed oil content of oilseed crop plants and oleogenous algae. Two other projects deal with the biochemistry and function of sphingolipids in plants and fungi as well as with wax ester forming enzymes. In addition we aim to identify chemical signals by metabolomics approaches that are exchanged during the infection between *Verticillium longisporum* and *Arabidopsis thaliana*.

Selected Recent Publications

Tarazona P, Feussner K, Feussner I (2015) An enhanced plant lipidomics method based on multiplexed liquid chromatography-mass spectrometry reveals additional insights into cold- and drought-induced membrane remodeling. Plant J 84(3): 621-33

Volkov A, Khoshnevis S, Neumann P, Herrfurth C, Wohlwend D,. Ficner R, Feussner I (2013) Crystal structure analysis of a fatty acid double-bond hydratase from *Lactobacillus acidophilus*. Acta Cryst D 69: 648-657

Djamei A, Schipper K, Rabe F, Ghosh A, Vincon V, Kahnt J, Osorio S, Tohge T, Fernie AR, Feussner I, Feussner K, Meinicke P, Stierhof YD, Schwarz H, Macek B, Mann M, Kahmann R (2011) Metabolic priming by a secreted fungal effector. Nature 478: 395-398

Address

Dept. of Molecular
Structural Biology
Institute for Microbiology
and Genetics & GZMB
University of Göttingen
Justus-von-Liebig-
Weg 11

37077 Göttingen
Germany

phone: +49-551-39 14072
fax: +49-551-39 14082
e-mail: rficner@gwdg.de

Further Information

www.uni-goettingen.de/msb

Ralf Ficner

Professor of Structural Biology

- Dr. rer. nat. (1992) and Postdoc (1993), Max Planck Institute for Biochemistry, Martinsried
- Postdoctoral fellow, EMBL Heidelberg, 1994 – 1996
- Junior Group Leader, University of Marburg, 1997 – 2000
- Appointed 2001 as Head of the Department of Molecular Structural Biology at the University of Göttingen

Major Research Interests

In order to understand the relationship between the three-dimensional structure and the cellular function of biological macromolecules we determine the structures of proteins and protein-RNA complexes by means of X-ray crystallography. Our current projects concern proteins involved in the splicing and modification of RNA and, as well, proteins required for the nucleocytoplasmic transport.

Selected Recent Publications

Fischer N, Neumann P, Konevega AL, Bock LV, Ficner R, Rodnina MV, Stark H (2015) Structure of the *E. coli* ribosome-EF-Tu complex at <3 Å resolution by Cs-corrected cryo-EM. Nature 520: 567-570

Kuhle B, Ficner R (2014) A monovalent cation acts as structural and catalytic cofactor in translational GTPases. EMBO J 33: 2547-2563

Neumann P, Lakomek K, Naumann P-T, Erwin W, Lauhon C, Ficner R (2014) Crystal structure of a 4-thiouridine synthetase - RNA complex reveals specificity of tRNA U8 modification. Nucleic Acids Res 42: 6673-6685

Kuhle B, Ficner R (2014) eIF5B employs a novel domain release mechanism to catalyze ribosomal subunit joining. EMBO J 33: 1177-1191

Ahmed YL, Gerke J, Park HS, Bayram O, Neumann P, Ni M, Dickmanns A, Kim SC, Yu JH, Braus GH, Ficner R (2013) The velvet family of fungal regulators contains a DNA-binding domain structurally similar to NF-kappaB. PLoS Biol 11: e1001750

Monecke T, Haselbach D, Voss B, Russek A, Neumann P, Thomson E, Hurt E, Zachariae U, Stark H, Grubmüller H, Dickmanns A, Ficner R (2013) Structural basis for cooperativity of CRM1 export complex formation. Proc Natl Acad Sci USA 110: 960-965

Khoshnevis S, Hauer F, Milon P, Stark H, Ficner R (2012) Novel insights into the architecture and protein interaction network of yeast eIF3. RNA 18: 2306-2319

Lehwess-Litzmann A, Neumann P, Parthier C, Lüdtke S, Golbik R, Ficner R, Tittmann K (2011) Twisted Schiff base intermediates and substrate locale revise transaldolase mechanism. Nat Chem Biol 7(10): 678-684

Güttler T, Madl T, Neumann P, Deichsel D, Corsini L, Monecke T, Ficner R, Sattler M, Gorlich D (2010) NES consensus redefined by structures of PKI-type and Rev-type nuclear export signals bound to CRM1. Nature Struct Mol Biol 17: 1367-1376

Schulz E-C, Dickmanns A, Urlaub H, Schmitt A, Mühlenhoff M, Stummeyer K, Schwarzer D, Gerardy-Schahn R, Ficner R (2010) Crystal structure of a novel intramolecular chaperone mediating triple ß-helix folding. Nature Struct Mol Biol 17: 210-215

Monecke T, Güttler T, Neumann P, Dickmanns A, Görlich D, Ficner R (2009) Crystal structure of the nuclear export receptor CRM1 in complex with Snurportin1 and RanGTP. Science 324(5930): 1087-91

Address

Laboratory of Chromatin Biochemistry
Max Planck Institute for Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 1340
fax: +49-551-201 1197
e-mail: wfischl@gwdg.de

Further Information

http://www.mpibpc.mpg.de/research/ags/fischle/

Wolfgang Fischle

Group Leader at the MPI for Biophysical Chemistry

- Dr. rer. nat. (PhD), University of Tübingen, Germany, 2001
- Graduate Research Fellow, The J. David Gladstone Institute (UCSF), San Francisco, CA, USA, 1997 – 2001
- Postdoctoral Fellow, The Rockefeller University, New York, NY, USA, 2001 – 2005
- Damon Runyon Cancer Research Fellow, 2002 – 2005
- Head of the Chromatin Biochemistry Group, Max Planck Institute for Biophysical
  Chemistry, Göttingen, Germany, since 2006

Major Research Interests

To sustain life in different environments cells and organisms must adjust to different conditions and external cues. In contrast to immediate and mostly transient responses to short-term stimuli, processes of long-term adaptation require lasting changes in gene expression patterns. Such epigenetic changes are controlled on the level of chromatin, the packaging form of eukaryotic genomes. Here, different DNA and histone modifications are associated with distinct functional states of chromatin.
Overall, our research aims to gain detailed, fundamental understanding of the processes that read and translate patterns of chromatin marks for mediating biological outcomes. Currently, we are tackling two main questions. A) How do histone modifications in conjunction with DNA methylation establish seemingly stable chromatin structures in response to internal and external cues? B) How do small cellular metabolites and signaling molecules tune the readout of chromatin marks? To address these problems we are constantly expanding our highly interdisciplinary approaches. These include advancing technologies for establishing and analyzing complex chromatin systems *in vitro* (biochemistry and biophysics), molecular and cellular biology for studying essential chromatin components and global analysis of modules of epigenetic regulation.
We strongly believe that by understanding the essential molecular control mechanisms of chromatin regulation we will ultimately be able to develop strategies for intervention of major diseases.

Selected Recent Publications

Fischle W, Schwarzer D, Mootz HD (2015) Chemical biology: Chromatin chemistry goes cellular. Nat Chem 7(5): 371-3

Kost N, Kaiser S, Ostwal Y, Riedel D, Stützer A, Nikolov M, Rathke C, Renkawitz-Pohl R, Fischle W (2015) Multimerization of *Drosophila* sperm protein Mst77F causes a unique condensed chromatin structure. Nucleic Acids Res 43(6): 3033-45

Gelato KG, Tauber M, Ong M, Winter S, Hiragami-Hamada K, Sindlinger J, Lemak A, Bultsma Y, Houliston S, Schwarzer D, Divecha N, Arrowsmith CH, Fischle W (2014) Interaction of UHRF1 with the unmodified or lysine 9 trimethylated H3 tail is allosterically regulated by phosphatidylinositol 5-phosphate. Mol Cell 54: 905-919

Wilkins BJ, Rall NA, Ostwal Y, Kruitwagen T, Hiragami-Hamada K, Winkler M, Barral Y, Fischle W, Neumann H (2014) A cascade of histone modifications induces chromatin condensation in mitosis. Science 343: 77-80

Shema-Yaacoby E, Nikolov M, Haj-Yahya M, Siman P, Allemand E, Yamaguchi Y, Muchardt C, Urlaub, H, Brik A, Oren M, Fischle W (2013) Systematic identification of proteins binding to chromatin-embedded ubiquitylated H2B reveals recruitment of SWI/SNF to regulate transcription. Cell Rep 4: 601-608

Seeliger D, Soeroes S, Klingberg R, Schwarzer D, Grubmüller H, Fischle W (2012) Quantitative Assessment of Protein Interaction with Methyl-Lysine Analogues by Hybrid Computational and Experimental Approaches. ACS Chem Biol 7: 150-154

Address

Dept. of General and Developmental Plant Physiology
Schwann-Schleiden Research Center
University of Göttingen
Julia-Lermontowa-Weg 3

37077 Göttingen
Germany

phone: +49-551-39 177821
fax.: +49-551-39 177829
e-mail: cgatz@gwdg.de

Further Information

http://www.uni-goettingen.de/de/311988.html

Christiane Gatz

Professor of Plant Molecular Biology

- Dr. rer. nat. (1985) at the Institute for Biochemistry, Technical University Darmstadt
- Postdoctoral fellow at the University of Wisconsin, Madison, USA (1985 – 1987)
- Habilitation in Molecular Genetics at the Freie Universität Berlin in 1992
- Professor at the University of Bielefeld (1993 – 1995)
- Alfried Krupp von Bohlen und Halbach-Award for young university professors (1994)
- Professor at the University of Göttingen since 1996

Major Research Interests

Our laboratory is interested in the molecular mechanisms establishing plant innate immunity. We focus on the elucidation of signal transduction mechanisms that lead to transcriptional reprogramming in the course of plant defense responses against bacteria and fungi. Plants have developed multiple layers of defense responses against pathogens. In general, infection of the model plant *Arabidopsis thaliana* with biotrophic pathogens (pathogens that exploit resources of living cells) leads to the activation of salicylic acid (SA)-mediated defense responses, whereas infection with necrotrophic pathogens (pathogens that kill cells to obtain access to nutrients) elicits jasmonic acid/ethylene (JA/ET)-dependent responses. If plants are infected by both types of pathogens, the SA pathway represses the JA/ET pathway (cross-talk). Members of the TGA family of transcription factors have been identified as essential regulators of both responses. These proteins reside in the cell in an inactive state before pathogen infection. We are interested in the SA-mediated mechanisms that activate TGA factors when they function as activators of the SA response (Fode et al., 2008). Moreover, we analyze, how these factors mediate the negative effect of SA on the JA/ET response (Zander et al., 2010; Zander et al 2012). In this context, we have identified the family of plant-specific ROXY-type glutaredoxins, which interact with TGA factors to influence defense responses (Ndamukong et al., 2007; Zander et al., 2012).
We combine genetic (e.g. analysis of mutants and double mutants), molecular (e.g. gene expression analysis by real-timer RT PCR), cell biological (subcellular localization and protein-protein interaction studies in living cells) and biochemical (e.g. chromatin immunoprecipitation) approaches to gain novel insights into these complex mechanisms.
A further project analyzes the function of the JA receptor COI1 in the defense against the vascular pathogen *Verticillium longisporum*. Whereas COI1 usually promotes defense responses against necrotrophic fungi when activated by JA, it promotes susceptibility independently from JA in response to infection with *V. longisporum* (Ralhan et al., 2012). Our aim is to understand the activation and the downstream effects of this novel COI1 function.

Selected Recent Publications

Gutsche N, Thurow C, Zachgo S, Gatz C (2015) Plant-specific CC-type glutaredoxins: functions in developmental processes and stress responses. Biol Chem 396(5): 495-509

Zander M, Thurow C, Gatz C (2014) TGA transcription factors activate the salicylic acid-suppressible branch of the ethylene-induced defense program by regulating ORA59 expression. Plant Physiol 65: 1671-1683

Ralhan A, Schottle S, Thurow C, Iven T, Feussner I, Polle A, Gatz C (2012) The vascular pathogen *Verticillium longisporum* requires a jasmonic acid-independent COI1 function in roots to elicit disease symptoms in *Arabidopsis* shoots. Plant Physiol 159: 1192-1203

Zander M, Chen S, Imkampe J, Thurow C, Gatz C (2011) Repression of the *Arabidopsis thaliana* jasmonic acid/ethylene-induced defense pathway by TGA-interacting glutaredoxins depends on their C-Terminal ALWL motif. Mol Plant 5: 831-40

Zander M, La Camera S, Lamotte O, Metraux JP, Gatz C (2010) *Arabidopsis thaliana* class-II TGA transcription factors are essential activators of jasmonic acid/ethylene-induced defense responses. Plant J 61: 200-210

Address

Dept. of Cellular Logistics
Max Planck Institute for
Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 2401
email: dgoerli@gwdg.de

Further Information

http://www.mpibpc.mpg.de/research/dep/goerlich/

Dirk Görlich

Professor, Director at the Max Planck Institute for Biophysical Chemistry

- 1989 Diploma (Biochemistry), Martin-Luther-Universität in Halle
- 1990 – 1993 Graduate studies (Laboratory of T.A. Rapoport, Berlin)
- 1993 Dr. rer. nat. (Biochemistry) Humboldt-Universität Berlin
- 1993 – 1995 Postdoc (Laboratory of R.A. Laskey, Cambridge, England)
- 1996 – 2007 Research group leader at the ZMBH Heidelberg
- 2001 – 2007 Professor for Molecular Biology (Universität Heidelberg)
- 2007 – Director, Dept. Cellular Logistics, MPI for Biophysical Chemistry, Göttingen

Major Research Interests

- Nuclear pore complexes, their function and assembly
- Hydrogels, “smart” materials, phase separations
- Structural biology
- Importins and Exportins, cargo recognition
- Recombinant antibodies, protein engineering

Selected Recent Publications

Chug H, Trakhanov S, Hülsmann BB, Pleiner T, Görlich, D (2015) Crystal structure of the metazoan Nup62•Nup58•Nup54 nucleoporin complex. Science 350(6256): 106-10

Schmidt HB, Görlich D (2015) Nup98 FG domains from diverse species spontaneously phase-separate into particles with nuclear pore-like permselectivity. eLife 4: e04251

Frey S, Görlich D (2014) A new set of highly efficient, tag-cleaving proteases for purifying recombinant proteins. J Chromatogr A 1337: 95-105

Samwer M, Dehne HJ, Spira F, Kollmar M, Gerlich DW, Urlaub H, Görlich D (2013) The nuclear F-actin interactome of *Xenopus* oocytes reveals an actin-bundling kinesin that is essential for meiotic cytokinesis. EMBO J 32: 1886-1902

Labokha AA, Gradmann S, Frey S, Hülsmann BB, Urlaub H, Baldus M, Görlich D (2013) Systematic analysis of barrier-forming FG hydrogels from *Xenopus* nuclear pore complexes. EMBO J 32: 204-218

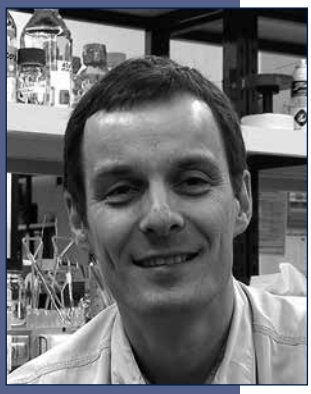
Hülsmann BB, Labokha A, Görlich D (2012) The permeability of reconstituted nuclear pores provides direct evidence for the selective phase model. Cell 150: 738-751

Güttler T, Madl T, Neumann P, Deichsel, D, Corsini, L, Monecke T, Ficner R, Sattler M, Görlich D (2010) NES consensus redefined by structures of PKI-type and Rev-type nuclear export signals bound to CRM1. Nat Struct Mol Biol 17: 1367-1376

Frey S, Görlich D (2009) FG/FxFG as well as GLFG repeats form a selective permeability barrier with self-healing properties. EMBO J 28: 2554-2567

Frey S, Görlich D (2007) A saturated FG-repeat hydrogel can reproduce the permeability properties of nuclear pore complexes. Cell 130: 512-523

Frey S, Richter, RP, Görlich D (2006) FG-rich repeats of nuclear pore proteins form a three-dimensional meshwork with hydrogel-like properties. Science 314: 815-817



Address

Dept. of NMB-based Structural Biology
Max Planck Institute for Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 2201
+49-551-201 2200
fax: +49-551-201 2202
email: cigr@nmr.mpibpc.mpg.de

Further Information

http://medusa.nmr.mpibpc.mpg.de/

Christian Griesinger

Professor, Director at the Max Planck Institute for Biophysical Chemistry, Göttingen

- Dr. phil. nat. University of Frankfurt (1986, Prof. Dr. H. Kessler)
- Postdoctoral Fellow at Lab. for Physical Chemistry, ETH Zürich (1986 – 1989, Prof. Dr. R. R. Ernst)
- Full Professor for Organic Chemistry at the University of Frankfurt (1990 – 2000)
- Appointed as Director at the Max Planck Institute for Biophysical Chemistry (1999)

Major Research Interests

In the department, we develop NMR spectroscopic methods and apply them to the investigation of water soluble and membrane proteins, nucleic acids and their complexes as well as drug/target complexes. We are specifically focussing on the dynamics of biomolecules. Structural biology projects are performed in the context of signal transduction, ion channels, cytoskeletal proteins, enzymes and drug/target complexes using NMR as well as X-ray crystallography to characterize structure and dynamics. An applied project is the investigation of proteins involved in neurodegenerative diseases that are studied in the context of the CNMPB and involve NMR and other biophysical methods as well as chemical synthesis. Methods developments are aimed at pushing the limits of sensitivity for NMR spectroscopic detection (e.g. DNP), developing the measurement of structurally and dynamically relevant parameters, establishing methods to describe structural ensembles for folded and intrinsically disordered proteins. For solid state NMR investigations, pulse sequences that allow structure determination of uniformly labelled membrane proteins as well as oligomers and fibrils formed from proteins involved in neurodegenerative diseases have been successfully developed.

Selected Recent Publications

Carneiro MG, Reddy JG, Griesinger C, Lee D (2015) Speeding-up exchange-mediated saturation transfer experiments by Fourier transform. J Biomol NMR [in press]

Wagner J, Ryazanov S, Leonov A, Levin J, Shi S, Schmidt F, Prix C, Pan-Montojo F, Bertsch U, Mitteregger-Kretzschmar G, Geissen M, Eiden M, Leidel F, Hirschberger T, Deeg AA, Krauth JJ, Zinth W, Tavan P, Pilger J, Zweckstetter M, Frank T, Bähr M, Weishaupt JH, Uhr M, Urlaub H, Teichmann U, Samwer M, Bötzel K, Groschup M, Kretzschmar H, Griesinger C, Giese A (2013) Anle138b: a novel oligomer modulator for disease-modifying therapy of neurodegenerative diseases such as prion and Parkinson's disease. Acta Neuropathol 125(6): 795-813

Honndorf V, Coudevylle N, Laufer S, Becker S, Griesinger C, Habeck M (2012) Inferential NMR/X-ray-based structure determination of a dibenzo[a,d]cycloheptenone inhibitor-p38a MAP kinase complex in solution. Angew Chem Int Ed 51: 2359-2362

Ban D, Funk M, Gulich R, Egger D, Sabo TM, Walter KFA, Bryn Fenwick R, Giller K, Pichierri F, de Groot BL, Lange OF, Grubmüller H, Salvatella X, Wolf M, Loidl A, Kree R, Becker S, Lakomek NA, Lee D, Lunkenheimer P, Griesinger C (2011) Kinetics of conformational sampling in ubiquitin. Angew Chem Int Ed 50: 11437-11440

Rodriguez-Castaneda F, Maestre-Martinez M. Coudevylle N, Dimova K, Junge H, Lipstein N, Lee D, Becker S, Brose N, Jahn O, Carlomagno T, Griesinger C (2010) Modular architecture of Munc13/calmodulin complexes: dual recognition by Ca^{2+} and possible function in short-term synaptic plasticity. EMBO J 29: 680-91

Lange O, Lakomek NA, Farès C, Schroeder GF, Walter K, Becker S, Meiler J, Grubmueller H, Griesinger C, de Groot BL (2008) Recognition dynamics up to microseconds revealed from an RDC-derived ubiquitin ensemble in solution. Science 320: 1471-1475

Bayrhuber M, Meins T, Habeck M, Becker S, Giller K, Villinger S, Vonrhein C, Griesinger C, Zweckstetter M, Zeth K (2008) Structure of the human voltage-dependent anion channel. Proc Natl Acad Sci USA 105: 15370-15375

Address

Department of Medical Microbiology
Medical Faculty of the University of Göttingen
Kreuzbergring 57

37075 Göttingen
Germany

phone: +49-551-39 5801/ 5806
fax: +49-551-39 5861
e-mail: ugross@gwdg.de

Further Information

http://www.bakteriologie.uni-goettingen.de/

Uwe Groß

Professor of Medical Microbiology

- M.D., University of Hamburg 1987
- Postdoctoral fellow, UC Los Angeles, California, 1987 – 1989
- Professor of Medical Parasitology, University of Würzburg 1998/1999
- Appointed 1999 as head of the Department of Medical Microbiology, University of Göttingen

Major Research Interests

The Department of Medical Microbiology is trying to understand infectious diseases by linking applied and basic sciences, e.g. aspects of epidemiology and pathogenesis. In regards to bacteriology, we are focusing on the intestinal pathogens *Campylobacter jejuni* and *Clostridium difficile*, where we use molecular approaches to identify and characterize virulence-associated factors, such as those involved in invasion (*Campylobacter*) or in spore regulation (*Clostridium*). In addition, the epidemiology of both pathogens in different regions and environments is under investigation.
Fungal infections caused by *Candida* and *Aspergillus* is a second major research topic. Like in bacterial infections, antimicrobial resistances are an emerging threat in mycology as well. Therefore, we focus on analyzing the epidemiology and the mechanisms of antifungal resistances.
The protozoan parasite *Toxoplasma gondii* usually causes asymptomatic infections in immunocompetent adults leading to lifelong persistence especially in the brain and in muscle tissue. Infections are especially dangerous during pregnancy and in immuno-compromised individuals (i. e. patients suffering from AIDS). We are interested in the epidemiology of toxoplasmosis as well as in the cross-talk between the parasite and its host cell on a molecular level. Here, we investigate how the parasite (i) modulates the host cell capacity for MHC-restricted antigen presentation and (ii) inhibits apoptosis of the infected cell. Both mechanisms allow intracellular persistence.
Recently, we also started to develop the theme Global Health in regards to infectious deiseases and cooperate with scientists from Ghana, Kenya, and Tanzania
In addition, we are appointed the National Reference Center for Systemic Mycoses. In this respect, we are investigating fungal factors and mechanisms that are involved in pathogenesis of mycoses; i.e. cell wall structure and differentiation processes.

Selected Recent Publications

Bader O, Weig M, Reichard U, Lugert R, Kuhns M, Christner M, Held J, Peter S, Schumacher U, Buchheidt D, Tintelnot K, Groß U and MykoLabNet-D Partners (2013) Cyp51A-based mechanisms of *Aspergillus fumigatus* azole drug resistance present in clinical samples from Germany. Antimicrobial. Agents Chemother 57: 3513-357

Zautner AE, Masanta WO, Tareen AM, Weig M, Lugert R, Groß U, Bader O (2013) Discrimination of multilocus sequence typing-based *Campylobacter jejuni* subgroups by MALDI-TOF mass spectrometry. BMC Microbiol 13(1): 247

Hotop A, Hlobil H, Groß U (2012) Efficacy of rapid treatment initiation following primary *Toxoplasma gondii* infection during pregnancy. Clin Infect Dis 54: 1545-52

Lin SS, Groß U, Bohne W (2011) Two internal type II NADH dehydrogenases of *Toxoplasma gondii* are both required for optimal tachyzoite growth. Mol Microbiol 82: 209-221

Groß U, Amuzu SK, de Ciman R, Kassimova I, Groß L, Rabsch W, Rosenberg U, Schulze M, Stich A, Zimmermann O (2011) Bacteremia and antibiotic drug resistance over time, Ghana. Emerg Infect Dis 17: 1879-1882

Address

Dept. of Developmental Biochemistry
University Medical Center Göttingen
Justus-von-Liebig-Weg 11

37077 Göttingen
Germany

phone: +49-551-39 14613
fax: +49-551-39 14614
e-mail: Joerg.grosshans@medizin.uni-goettingen.de

Further Information

http://www.gwdg.de/~jgrossh/
http://www.uni-goettingen.de/en/105241.html

Jörg Großhans

Professor of Developmental Biochemistry

- 1993 Diplom Biochemistry, Tübingen
- 1993 – 1996 Doctoral research with C Nüsslein-Volhard, Max-Planck-Institut für Entwicklungsbiologie, Tübingen
- 1997 – 2001 Post-doc with E Wieschaus, Princeton (USA)
- 2002 – 2008 ZMBH and Emmy-Noether research group, Heidelberg
- since 2009 Professor, Universitätsmedizin Göttingen

Major Research Interests

Biological structure formation and ageing.
Our group is interested in the molecular and cell-biological mechanisms how biological structures are formed. We analyse structure formation in the early *Drosophila* embryo employing genetical, biochemical and embryological experiments as well as live-imaging. Specifically we investigate how nuclear shape is determined and how the farnesylated protein Kugelkern is involved, how the cells are regularly arranged, how apical-basal polarity is established and how the number of synchronous cell divisions is robustly controlled. Based on our studies nuclear shape we have studied the function of the nuclear lamina and lamina proteins, such as lamin and Kugelkern, in ageing and stem cell proliferation and differentiation in the adult fly.

Selected Recent Publications

Winkler F, Gummalla M, Künneke L, Lv Z, Zippelius A, Aspelmeier T, Großhans J (2015) Fluctuation analysis of centrosomes reveals a cortical function of Kinesin-1. Biophysical Journal 109(5): 856-68

Wessel AD, Gummalla M, Grosshans J, Schmidt CF (2015) The mechanical properties of early *Drosophila* embryos measured by high-speed video microrheology. Biophysical Journal 108: 1899-1907

Zhang Y, Kong D, Reichl L, Vogt N, Wolf F, Großhans J (2014) The glucosyltransferase Xiantuan of the endoplasmic reticulum specifically affects E-Cadherin expression and is required for gastrulation movements in *Drosophila*. Dev Biol 390: 208-220

Acharya S, Laupsien P, Wenzl C, Yan S, Großhans J (2014) Function and dynamics of slam in furrow formation in early *Drosophila* embryo. Dev Biol 386: 371-384

Schulz O, Pieper C, Hähnel D, Clever M, Pfaff J, Kehlenbach RH, Wouters FS, Großhans J, Bunt G, Enderlein J (2013) Resolution-doubling in fluorescence microscopy with Confocal Spinning-Disk Image Scanning Microscopy. PNAS 110: 21000-21005.

Yan S, Lv Z, Winterhoff M, Wenzl C, Zobel T, Faix J, Bogdan S, Grosshans J (2013) The F-BAR protein Cip4/Toca-1 antagonizes the formin Diaphanous in membrane stabilization and compartmentalization. J Cell Sci 126: 1796-1805

Sung HW, Spangenberg S, Vogt N, Grosshans J (2013) Number of nuclear divisions in the *Drosophila* blastoderm controlled by onset of zygotic transcription. Curr Biol 23: 133-138

Albrecht SC, Barata A, Grosshans J, Teleman AA, Dick TP (2011). *In vivo* mapping of hydrogen peroxide and oxidaized glutathione reveals chemical and regional specificity of redox homeostasis. Cell Metab 14: 819-29

Address

Dept. of Theoretical and Computational Biophysics
Max Planck Institute for Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 2300/ 2301
fax: +49-551-201 2302
e-mail: hgrubmu@gwdg.de

Further Information

http://www.mpibpc.mpg.de/home/grubmueller/index.html

Helmut Grubmüller

Professor, Director at the Max Planck Institute for Biophysical Chemistry

- 1994 Dr. rer nat. (Physics), Technical University of Munich
- 1997 EMBO fellow at the Institute for Molecular Biology and Biophysics, Federal Institute of Technology (ETH) Zurich, Switzerland
- 1998 – 2003 Head of the Theoretical Molecular Biophysics Group at the Max Planck Institute for Biophysical Chemistry, Göttingen
- 2003 Associate Professor for Biomolecular Sciences at the École Polytechnique Fédérale de Lausanne (EPFL)
- 2003 - Director at the Max Planck Institute for Biophysical Chemistry, Göttingen, Head of the Theoretical and Computational Molecular Biophysics Department
- 2005 - Honorary Professor for Physics at the University of Göttingen

Major Research Interests

The question 'How do proteins work?' is our driving force. We study biomolecular dynamics and function by atomistic molecular dynamics and qm/mm simulations. Emphasis is on protein function, as well as on protein/DNA/RNA interactions.
Available projects address nuclear pore transport, the ribosome, molecular motors such as F-ATPase, protein unfolding as well as the interaction with radiation with a focus at single molecules, typically in close collaboration with experimental groups. The simulation of single molecule AFM experiments by force probe techniques helps us to reveal mechanisms of proteins function involving mechanical stress such as the muscular force sensor titin kinase, and so do improved methods to calculate thermodynamic quantities from simulations. We are continuously advancing our simulation techniques and scalability on massively parallel computers. The group of ca. 20 PhD students and postdocs shares a strong background mainly in physics, and scientific computing, but also in chemistry and biology. We enjoy exclusive access to a high-performance linux cluster of ca. 3000 processor cores.

Selected Recent Publications

Bock LV, Blau C, Vaiana AC, Grubmüller H (2015) Dynamic contact network between ribosomal subunits enables rapid large-scale rotation during spontaneous translocation. Nucleic Acids Res 43(14): 6747-60

Risselada HJ, Bubnis G, Grubmüller H (2014) Expansion of the fusion stalk and its implication for biological membrane fusion. Proc Natl Acad Sci USA 111(30): 11043-8

Czub J, Grubmüller H (2014) Rotation triggers nucleotide-independent conformational transition of the empty βsubunit of FβATPase. J Am Chem Soc 136(19): 6960-8

Bock LV, Blau C, Schröder GF, Davydov II, Fischer N, Stark H, Rodnina MV, Vaiana AC, Grubmüller H (2013) Energy barriers and driving forces in tRNA translocation through the ribosome. Nat Struct Mol Biol 20(12): 1390-6

Czub J, Grubmüller H (2011) Torsional elasticity and energetics of F1-ATPase. Proc Natl Acad Sci USA 108(18): 7408-7413

Lange OF, Lakomek NA, Fares C, Schröder GF, Walter KFA, Becker S, Meiler J, Grubmüller H, Griesinger C, de Groot BL (2008) Recognition dynamics up to microseconds revealed from an RDC-derived ubiquitin ensemble in solution. Science 320: 1471-1475

Sieber JJ, Willig KI, Kutzner C, Gerding-Reimers C, Harke B, Donnert G, Rammner B, Eggeling C, Hell SW, Grubmüller H, Lang T (2007) Anatomy and dynamics of a supramolecular membrane protein cluster. Science 317: 1072-1076

Address

Department of Human Genetics
Section of Developmental Genetics
University Medical Center Göttingen
Heinrich-Düker-Weg 12

37073 Göttingen
Germany

phone: +49-551-39 14010
fax: +49-551 39 6580
e-mail: hhahn@gwdg.de

Further Information

http://www.uni-goettingen.de/en/57976.html

Heidi Hahn

Professor of Molecular Developmental Genetics

- Dr. med., University of Würzburg, 1992
- Postdoctoral Fellow, National Institutes of Health, Bethesda, Maryland, USA (1993 – 1998)
- Junior Group Leader (BioFuture), Technical University of Munich (1999 – 2000)
- Professor of Molecular Developmental Genetics, University of Göttingen since 2001

Major Research Interests

Cancer is a disease that results from inappropriate cell division induced by hyperproliferation. In many cases, the development of cancer is associated with genes or signaling pathways important for patterning during embryogenesis.
We investigate the role of the Hedgehog/Patched (Hh/Ptch) signaling cascade in the development of solid tumors. The focus is on rhabdomyosarcoma and basal cell carcinoma. In addition, we are investigating the role of Hh/Ptch signaling in cutaneous squamous cell carcinoma and adenoma of the pituitary gland.
The first aim is the discovery of molecular and cellular events that trigger the initiation of Ptch associated tumors. The second aim is to elucidate the function of Hh signaling during tumor progression. The current focus is on the interaction between Hh/Ptch and Wnt signaling, and on Hh/Ptch and Ras signaling during formation and progression of basal cell carcinoma and rhabdomyosarcoma. The third goal is the identification of drugs that target Hh/Ptch-associated solid tumors. Currently we are analyzing the anti-tumoral effects of several Hh inhibitors in combination with drugs targeting the Ras/Mek/Erk and PI3K/Akt/mTor signaling cascades. To test the anti-tumor activity of the drugs we use tumor-bearing Ptch mutant mice.

Selected Recent Publications

Nitzki F, Cuvelier N, Dräger J, Schneider A, Braun T, Hahn H (2015) Hedgehog/Patched-associated rhabdomyosarcoma formation from Delta1-expressing mesodermal cells. Oncogene [in press]

Uhmann A, Heß I, Frommhold A, König S, Zabel S, Nitzki F, Dittmann K, Lühder F, Christiansen H, Reifenberger J, Schulz-Schaeffer W, Hahn H (2014) DMBA/TPA treatment is necessary for BCC formation from Patched deficient epidermal cells in Ptchflox/floxCD4Cre+/- mice. J Invest Dermatol 134: 2620-2629

Pelczar P, Zibat Z, van Dop WA, Heijmans J, Bleckmann A, Gruber W, Nitzki F, Uhmann A, Guijarro MV, Hernando E, Dittmann K, Wienands J, Dressel R, Wojnowski L, Binder C, Taguchi T, Beissbarth T, Hogendoorn PCW, Antonescu CR, Rubin BP, Schulz-Schaeffer W, Aberger F, van den Brink GR, Hahn H (2013) Inactivation of patched1 in mice leads to development of gastrointestinal stromal-like tumors that express pdgfrα but not kit. Gastroenterology 144(1): 134 -144.e6

Nitzki F, Zibat A, Frommhold A, Schneider A, Schulz-Schaeffer W, Braun T, Hahn H (2011) Uncommitted precursor cells might contribute to increased incidence of embryonal rhabdomyosarcoma in heterozygous Patched1 mutant mice. Oncogene 30: 4428-36

Nitzki F, Zibat A, Konig S, Wijgerde M, Rosenberger A, Brembeck F, Carstens PO, Frommhold A, Uhmann A, Klingler S, Reifenberger J, Pukrop T, Aberger F, Schulz-Schaeffer W, Hahn H (2010) Tumor stroma-derived Wnt5a induces differentiation of basal cell carcinoma of Ptch mutant mice via CaMKII. Cancer Research 70: 2739-48

Uhmann A, Dittmann K, Nitzki F, Dressel R, Koleva M, Frommhold A, Zibat A, Binder C, Adham I, Nitsche M, Heller T, Armstrong V, Schulz-Schaeffer W, Wienands J, Hahn H (2007) The Hedgehog receptor Patched controls lymphoid lineage commitment. Blood 110: 1814-23

Hahn H, Wicking C, Zaphiropoulos P, Gailani M, Shanley S, Chidambaram A, Vorechovsky I, Holmberg E, Unden A, Gillies S, Negus K, Smyth I, Pressman C, Leffell D, Gerrard B, Goldstein A, Wainright B, Toftgard R, Chenevix-Trench G, Dean M, Bale A (1996) Mutations of the human homologue of *Drosophila* patched in the nevoid basal cell carcinoma syndrome. Cell 85: 841-51

Address

Dept. of NanoBiophotonics
Max Planck Institute for
Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 2501
fax: +49-551 201 2505
e-mail: shell@gwdg.de

Further Information

http://www.mpibpc.mpg.de/groups/hell/

Stefan Hell

Professor, Director at the Max Planck Institute for Biophysical Chemistry

- 1987 Diploma in Physics, University of Heidelberg (1.0)
- 1990 Doctorate in Physics, University of Heidelberg (summa cum laude)
- 1991 – 1993 Postdoctoral Researcher, EMBL (European Molecular Biology Laboratory)
- 1993 – 1996 Principal Investigator, Laser Microscopy Group; University of Turku, Finland
- 1996 Habilitation in Physics, University of Heidelberg; Physics teaching since 02/1996
- 1997 – 2002 Head, Max-Planck Junior Group High Resolution Optical Microscopy, at the Max Planck Institute for Biophysical Chemistry Göttingen, Germany
- since 10/2002 Director at the Max Planck Institute for Biophysical Chemistry, Head of Department of NanoBiophotonics
- since 12/2003 Apl. Prof., Faculty of Physics, University of Heidelberg
- since 12/2003 Head of High Resolution Optical Microscopy Division, DKFZ Heidelberg
- since 01/2004 Hon. Prof., Faculty of Physics, University of Göttingen
- 2014 The Nobel Prize in Chemistry

Major Research Interests

Optical microscopy beyond the diffraction barrier with far-field optics. Invention of STED, RESOLFT, GSDIM and 4Pi microscopy and related techniques.

Selected Recent Publications

Ta H, Keller J, Haltmeier M, Saka SK, Schmied J, Opazo F, Tinnefeld P, Munk A, Hell SW (2015) Mapping molecules in scanning far-field fluorescence nanoscopy. Nat Commun 6: 7977

Schneider J, Zahn J, Maglione M, Sigrist SJ, Marquard J, Chojnacki J, Kräusslich HG, Sahl SJ, Engelhardt J, Hell SW (2015) Ultrafast, temporally stochastic STED nanoscopy of millisecond dynamics. Nat Methods 12(9): 827-30

Hanne J, Falk HJ, Görlitz F, Hoyer P, Engelhardt J, Sahl SJ, Hell SW (2015) STED nanoscopy with fluorescent quantum dots. Nat Commun 6: 7127

Kolmakov K, Hebisch E, Wolfram T, Nordwig LA, Wurm CA, Ta H, Westphal V, Belov VN, Hell SW (2015) Far-Red Emitting Fluorescent Dyes for Optical Nanoscopy: Fluorinated Silicon-Rhodamines (SiRF Dyes) and Phosphorylated Oxazines. Chemistry 21(38): 13344-56

Hell SW (215) Nanoscopy with Focused Light (Nobel Lecture). Angew Chem Int Ed Engl 54(28):8054-66

Berning S, Willig KI, Steffens H, Dibaj P, Hell SW (2012) Nanoscopy in a Living Mouse Brain. Science 335: 551

Liu KSY, Siebert M, Mertel S, Knoche E, Wegener S, Wichmann C, Matkovic T, Muhammad K, Depner H, Mettke C, Bückers J, Hell SW, Müller M, Davis GW, Schmitz D, Sigrist SJ (2011) RIM-binding protein, a central part of the active zone, is essential for neurotransmitter release. Science 334: 1565-1569

Eggeling C, Ringemann C, Medda R, Schwarzmann G, Sandhoff K, Polyakova S, Belov VN, Hein B, von Middendorff C, Schönle A, Hell SW (2009) Direct observation of the nanoscale dynamics of membrane lipids in a living cell. Nature 457: 1159-1163

Willig KI, Rizzoli SO, Westphal V, Jahn R, Hell SW (2006) STED-microscopy reveals that synaptotagmin remains clustered after synaptic vesicle exocytosis. Nature 440: 935-939

Address

Dept. of Molecular Microbiology and Genetics
University of Göttingen
Grisebachstraße 8

37077 Göttingen
Germany

phone: +49-551-39 3815
fax: +49-551 39 3330
e-mail: kheimel@gwdg.de

Further Information

http://www.uni-goettingen.de/de/434133.html

Kai Heimel

Professor for Microbial Cell Biology

- Since 04/2012: Junior Professor for Microbial Cell Biology, Georg-August-University Göttingen
- 2012: Teaching stand-in for W3 Professorship of Genetics and Cell Biology, Karlsruhe Institute of Technology (KIT)
- 2010 – 2011: Postdoctoral fellow at the Karlsruhe Institute of Technology (KIT)
- 2010: Dr. rer. nat., Philipps-University Marburg
- 2005 – 2010: Doctoral thesis, Max-Planck Institute for Terrestrial Microbiology, Marburg and Karlsruhe Institute of Technology (KIT) (Germany)
- 2000 – 2005: Diploma (Biology), Philipps-University Marburg (Germany)

Major Research Interests

Research in our laboratory is focused on the Unfolded Protein Response (UPR) in development and disease signaling. Cells need to re-adjust and modify their cellular programs in response to a wide range of biotic and abiotic stimuli. The UPR is a highly conserved cellular response to maintain homeostasis of the endoplasmic reticulum (ER). In situations of increased demands for protein production and secretion, potentially harmful un- or mis-folded proteins accumulate in the ER and activate the UPR pathway. Defects in UPR signaling are associated with a wide range of developmental, metabolic and neurodegenerative disorders. Besides the role as a cellular stress response, recent work demonstrated that the UPR pathway is also involved in control of developmental processes. We uncovered that UPR signaling in the phytopathogenic fungus Ustilago maydis is required for disease development and directly coupled to the pathways that control parasitic growth of the fungus. Our future studies will aim to characterize these connections on a molecular level and further explore the role of UPR signaling in controlling cellular behavior and responses to different environments.

Selected Recent Publications

Lo Presti L, López Díaz C, Turrà D, Di Pietro A, Hampel M, Heimel K, Kahmann R (2015) A conserved co-chaperone is required for virulence in fungal plant pathogens. New Phytol [Epub ahead of print]

Heimel K (2015) Unfolded protein response in filamentous fungi - Implications in biotechnology. Appl Mircobiol Biotechnol 99: 121-132

Kellner N, Heimel K, Obhof T, Finkernagel F, Kämper J (2014) The SPF27 homologue Num1 connects splicing and kinesin 1-dependent cytoplasmic trafficking in *Ustilago maydis*. PLoS Genetics 10: e1004046; featured in Faculty of 1000 prime

Heimel K., Freitag J., Hampel M., Ast J, Bölker M., Kämper J (2013) Crosstalk between the Unfolded Protein Response and Pathways That Regulate Pathogenic Development in *Ustilago maydis*. Plant Cell 25: 4262-4277

Heimel K, Scherer M, Schuler D, Kämper J (2010) The Ustilago maydis Clp1 Protein Orchestrates Pheromone and b-Dependent Signaling Pathways to Coordinate the Cell Cycle and Pathogenic Development. Plant Cell (8): 2908-22

Heimel K*, Scherer M*, Vranes M, Wahl R, Pothiratana C, Schuler D, Vincon V, Finkernagel F, Flor-Parra I, Kämper J (2010) The transcription factor Rbf1 is the master regulator for bmating type controlled pathogenic development in *Ustilago maydis*. PLoS Pathog 6(8): e1001035 (*equal contribution)

Zahiri A*, Heimel K*, Wahl R, Rath M, Kämper J (2010) The Ustilago maydis Forkhead Transcription Factor Fox1 Is Involved in the Regulation of Genes Required for the Attenuation of Plant Defenses During Pathogenic Development. Mol Plant Microbe Interact 18(9): 1118-29 (*equal contribution)

Address

Institute for Organic and Biomolecular Chemistry
University of Göttingen
Tammannstr. 2

37077 Göttingen
Germany

phone: +49-551-201 1685
fax: +49-551-201 1680
e-mail: claudia.hoebartner@mpibpc.mpg.de

Further Information

https://www.uni-goettingen.de/en/507570.html

Claudia Höbartner

Professor, Institute for Organic and Biomolecular Chemistry

- Dr. rer. nat. (PhD), University of Innsbruck, Austria, 2004
- Erwin Schrödinger postdoctoral Fellowship, FWF (Austrian Science Fund),
- University of Illinois at Urbana-Champaign, USA, 2005 – 2007
- Hertha Firnberg Fellowship, funded by FWF & bmwf (federal ministry of science and research), University of Innsbruck, Austria, 2007 – 2008
- Independent Research Group Leader, Max Planck Institute for Biophysical Chemistry, Göttingen, Germany, since 2008
- Professor at the Institute for Organic and Biomolecular Chemistry, University of Göttingen, since 2014

Major Research Interests

The work in our group is focused on the chemistry and biochemistry of natural and artificial nucleic acids, with special emphasis on functional and structural properties of catalytic DNA and modified RNA. Deoxyribozymes, also known as DNA enzymes or DNA catalysts, are single-stranded DNAs that are identified by *in vitro* selection from random-sequence DNA pools. Most prominent reactions catalyzed by DNA site-specific cleavage and ligation of RNA in different topologies. Catalytically active DNA molecules must fold into complex, three-dimensional structures that form the basis for their sophisticated functions. However, little is known about the molecular details of these structures and the mechanistic principles of DNA catalysis. We seek molecular level insights into the function and mechanism of DNA catalysts and approach these fundamental questions by a variety of chemical and biophysical methods. In this context, we developed reliable probing methods for the identification of critical molecular features for DNA catalysis. Other objectives are to demonstrate that DNA has the potential for novel chemical and biochemical catalysis and to apply deoxyribozymes for practical use. We explore the diversity of DNA-catalyzed reactions in as-yet unaddressed areas and develop nucleic acids as tools for post-synthetic modifications, such as site-specific attachment of fluorescent labels or other biophysical probes in DNA and RNA. We also study natural nucleic modifications, such as nucleobase and ribose methylations, and we use artificial nucleoside analogs, such as spin-labeled, fluorescent and caged nucleosides as probes for the investigation of RNA structure and function. We apply synthetic organic chemistry for generating modified nucleoside building blocks and use solid-phase synthesis, post-synthesis derivatization, enzymatic synthesis of RNA fragments and chemical and enzymatic ligation strategies for the preparation of complex RNA targets. The structural and biophysical properties of highly functionalized RNAs and their interactions with proteins are studied in collaboration with several other research groups at the Max Planck Institute for Biophysical Chemistry.

Selected Recent Publications

Javadi-Zarnaghi F, Höbartner C (2015) Functional Hallmarks of a Catalytic DNA that Makes Lariat RNA. Chemistry. [Epub ahead of print]

Wawrzyniak-Turek K, Höbartner C (2014) Enzymatic combinatorial nucleoside deletion scanning mutagenesis of functional RNA. Chem Commun (Camb) 50(75):1 0937-40

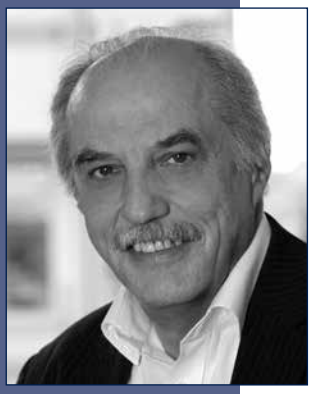
Büttner L, Javadi-Zarnaghi F, Höbartner C (2014) Site-specific labeling of RNA at internal ribose hydroxyl groups: terbium-assisted deoxyribozymes at work. J Am Chem Soc 136: 8131-7

Javadi-Zarnaghi F, Höbartner C (2013) Lanthanide cofactors accelerate DNA-catalyzed synthesis of branched RNA. J Am Chem Soc 135: 12839-12848

Büttner L, Seikowski J, Wawrzyniak K, Ochmann A, Höbartner C (2013) Synthesis of spin-labeled riboswitch RNAs using convertible nucleosides and DNA-catalyzed RNA ligation. Bioorg Med Chem 21: 6171-6180

Samanta B, Höbartner C (2013) Combinatorial Nucleoside-Deletion-Scanning Mutagenesis of Functional DNA. Angew Chem Int Ed 52: 2995-2999

Wachowius F, Höbartner C (2011) Probing essential nucleobase functional groups in aptamers and deoxyribozymes by nucleotide analog interference mapping of DNA, J Am Chem Soc 133: 14888-14891



Address

Dept. of Molecular
Developmental Biology
Max Planck Institute for
Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 1482
fax: +49-551-201 1755
e-mail: hjaeckl@gwdg.de

Further Information

http://www.mpibpc.mpg.de/groups/jaeckle

Herbert Jäckle

Professor, Director at the Max Planck Institute for Biophysical Chemistry

- Faculty member at the EMBL, Heidelberg (1980 – 1982)
- Head of the group (associate professor), Max Planck Institute for Develop mental Biology, Tübingen (1982 – 1988)
- Professor and Chairman, Dept. of Genetics and Microbiology, Univ. of Munich (1988 – 1991)
- Director, Dept. of Molecular Developmental Biology, Max Planck Institute for Biophysical Chemistry, Göttingen
- Vice-President of the Max Planck Society

Major Research Interests

Our research interest is focused on molecular processes and the mechanisms involved in the phenonenon of biological pattern formation during Drosophila embryogenesis. Aim of my studies is a better understanding of the biochemical pathways and the molecular characterization of the regulatory networks leading to the establishment of the segmental organization of the embryo, organ formation and cell behaviour underlying morphogenesis. Recent work concerns the genetic basis for energy homeostasis in cells.

Selected Recent Publications

Baumbach J, Hummel P, Bickmeyer I, Kowalc KM, Frank M, Knorr K, Hildebrandt A, Riedel D, Jäckle H, Kühnlein R (2014) A *Drosophila in vivo* screen identifies store-operated calcium entry as a key regulator of adiposity. Cell metabolism 19: 331-343

Günesdogan U, Jäckle H, Herzig A (2014) Histone supply regulates S phase timing and cell cycle progression. eLife, 3: e02443

Pengelly KAR, Copur Ö, Jäckle H, Herzig A, Müller J (2013) A Histone Mutant Reproduces the Phenotype Caused by Loss of Histone-Modifying Factor Polycomb. Science 339: 698-699

Beller M, Bulankina AV, Hsiao H-H, Urlaub H, Jäckle H, Kühnlein RP (2010) Perilipin-dependent Control of Lipid Droplet Structure and Fat Storage in *Drosophila*. Cell Metabolism 12: 521-532

Günesdogan U, Jäckle H, Herzig A (2010) A genetic system to assess *in vivo* the functions of histones and histone modifications in higher eukaryotes. EMBO reports 10: 772-776

Löhr U, Chung HR, Beller M, Jäckle H (2009) Anterior patterning in *Drosophila* does not depend on the Bicoid morphogen gradient. Proc Natl Acad Sci USA 51: 21695-21700

Address

Dept. of Neurobiology
Max Planck Institute for
Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 1635
fax: +49-551-201 1639
e-mail: rjahn@gwdg.de

Further Information

http://www.mpibpc.gwdg.de/abteilungen/190/

Reinhard Jahn

Professor, Director at the Max Planck Institute for Biophysical Chemistry

- Dr. rer. nat. 1981, University of Göttingen
- Assistant Professor, The Rockefeller University, New York (USA) 1985
- Junior Group leader, Max Planck Institute for Psychiatry, Martinsried, 1986
- Associate Professor of Pharmacology and Cell Biology, Yale University, and Investigator, Howard Hughes Medical Institute, New Haven (USA) 1991
- Professor of Pharmacology and Cell Biology, Yale University, New Haven, 1995
- Director, Max Planck Institute for Biophysical Chemistry, Göttingen, 1997

Major Research Interests

Our group is interested in the mechanisms of membrane fusion, with the main emphasis on regulated exocytosis in neurons. Intracellular membrane fusion events are mediated by a set of conserved membrane proteins, termed SNAREs. For fusion to occur, complementary sets of SNAREs need to be present on both of the fusing membranes, which then assemble in a zipper-like fashion to initiate membrane merger. The neuronal SNAREs are among the best characterized. They are the targets of the toxins responsible for botulism and tetanus, and they are regulated by several addtional proteins including synaptotagmin, the calcium sensor for neurotransmitter release. To understand how these proteins mediate fusion, we study their properties *in vitro* with biochemical and biophysical approaches using native and artificial membranes.
In a second set of projects, we use modern techniques such as quantitative proteomics to better understand supramolecular protein complexes involved in synaptic function. Using our quantitative description of synaptic vesicles as point of departure we aim at unraveling presynaptic protein networks involved in synaptic vesicle docking and fusion. Furthermore, we are studying regulation of presynaptic function by small GTPases and by protein phosphorylation.

Selected Recent Publications

Ryo J-K, Min D, Rah S-H, Kim SJ, Park Y, Kim H, Kim H-M, Jahn R*, Yoon T-Y* (2015) Spring-loaded unraveling of a single SNARE complex by NSF in one round of ATP turnover. Science 347: 1485-1489 (*corresponding authors)

Binotti B, Pavlos NJ, Riedel D, Wenzel D, Vorbrüggen G, Schalk AM, Kühnel K, Boyken J, Erck C, Martens H, Chua JJE, Jahn R (2015) The GTPase Rab26 links synaptic vesicles to the autophagy pathway. eLife 4: e05597

Honigmann A, van den Bogaart G, Iraheta E, Risselada HJ, Milovanovic D, Mueller V, Müllar S, Diederichsen U, Fasshauer D, Grubmüller H, Hell SW, Eggeling C, Kühnel K, Jahn R (2013) Phosphatidylinositol 4,5-bisphosphate clusters act as molecular beacons for vesicle recruitment. Nat Struct Mol Biol 20: 679-686

Park Y, Hernandez JM, van den Bogaart G, Ahmed S, Holt M, Riedel D, Jahn R (2012) Controlling synaptotagmin activity by electrostatic screening. Nature Struct Mol Biol 19: 991-997

Jahn R, Fasshauer D (2012) Exocytosis of synaptic vesicles – molecular machines, calcium, and beyond (review). Nature 490(7419): 201-7

Hernandez JM, Stein A, Behrmann E, Riedel D, Cypionka A, Farsi Z, Walla PJ, Raunser S, Jahn R (2012) Membrane fusion intermediates *via* directional and full assembly of the SNARE complex. Science 336: 1581-1584

Chua JJ, Butkevich E, Worseck JM, Kittelmann M, Gronborg M, Behrmann E, Stelzl U, Pavlos NJ, Lalowski M, Eimer S, Wanker EE, Klopfenstein DR*, Jahn R* (2012) Phosphorylation-regulated axonal dependent transport of syntaxin 1 is mediated by a Kinesin-1 adapter. Proc Natl Acad Sci USA 109: 5862-5867

van den Bogaart G, Meyenberg K, Risselada JH, Amin H, Willig KI, Hubrich BE, Dier M, Hell SW, Grubmüller H, Diederichsen U, Jahn R (2011) Membrane protein sequestering by ionic protein-lipid interactions. Nature 479: 552-555

Address

Dept. of NanoBiophotonics
Mitochondrial Structure and Dynamics group
Max Planck Institute for Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 2531
fax: +49-551-201 2505
e-mail: sjakobs@gwdg.de

Further Information

http://www.mpibpc.mpg.de/groups/jakobs/

Stefan Jakobs

Professor of High Resolution Microscopy in Neurodegenerative Diseases

- 1995 – Diploma, University of Kaiserslautern
- 1995 – 1999 Graduate studies (MPI for Plant Breeding Research, Cologne, Germany and John-Innes-Centre, Norwich, GB)
- 1999 Dr. rer. nat. University of Cologne
- 1999 Postdoc (Laboratory of J. Schell/K. Palme, MPI for Plant Breeding Research, Cologne)
- 1999 – 2005 Postdoc (MPI for Biophysical Chemistry, Laboratory of S.W. Hell)
- 2005 – Research group leader at the MPI for Biophysical Chemistry
- 2007 Habilitation (Botany/Cell Biology) at the Georg-August-University Göttingen
- 2010 – Professor (W2) of High Resolution Microscopy in Neurodegenerative Diseases, University of Göttingen Medical School, Dept. of Neurology

Major Research Interests

Our two major research interests are the investigation of the nanoscale architecture and dynamics of mitochondria and the analysis of reversibly switchable fluorescent proteins (RSFPs) as probes for super-resolution microscopy. Mitochondria are essential organelles in all eukaryotic cells and their dysfunction is involved in many devastating (neurodegenerative) diseases. We want to understand the organization of mitochondria on the nanoscale in healthy and challenged cells and investigate the molecular mechanisms that determine their intricate structure. We utilize a wide array of techniques, including molecular biology, biochemical methods as well as electron and super-resolution microscopy.
RSFPs are fluorescent proteins that may be switched by light between a non-fluorescent and a fluorescent state. Their unique properties open up numerous applications in microscopy and cell biology. We investigate the molecular switching mechanisms and aim to improve the properties of these fascinating proteins as probes for live-cell super-resolution microscopy.

Selected Recent Publications

Jans DC, Wurm CA, Riedel D, Wenzel D, Stagge F, Deckers M, Rehling P, Jakobs S (2013) STED super-resolution microscopy reveals an array of MINOS clusters along human mitochondria. Proc Natl Acad Sci USA 110: 8936-41

Grotjohann T, Testa I, Leutenegger M, Bock H, Urban NT, Lavoie-Cardinal F, Willig KI, Eggeling C, Jakobs S*, Hell SW* (* shared corresponding authors) (2011) Diffraction-unlimited all-optical imaging and writing with a photochromic GFP. Nature 478: 204-208

Brakemann T, Stiel AC, Weber G, Andresen M, Testa I, Grotjohann T, Leutenegger M, Plessmann U, Urlaub H, Eggeling C, Wahl MC, Hell SW, Jakobs S (2011) A reversibly photoswitchable GFP-like protein with fluorescence excitation decoupled from switching. Nature Biotech 29(10): 942-947

Kukat C, Wurm CA, Spåhr H, Falkenberg M, Larsson N, Jakobs S (2011) Super-resolution microscopy reveals that mammalian mitochondrial nucleoids have a uniform size and frequently contain a single copy of mtDNA. Proc Natl Acad Sci USA 108(33): 13534-9

Wurm CA, Neumann D, Lauterbach MA, Harke B, Egner A, Hell SW, Jakobs S (2011) Nanoscale distribution of mitochondrial import receptor Tom20 is adjusted to cellular conditions and exhibits an inner-cellular gradient. Proc Natl Acad Sci USA 108(33): 13546-51

Andresen M, Stiel AC, Fölling J, Wenzel D, Schönle A, Egner A, Eggeling C, Hell SW, Jakobs S (2008) Photoswitchable fluorescent proteins enable monochromatic multilabel imaging and dual color fluorescence nanoscopy. Nature Biotech 26: 1035-1040

Address

Institute for Physical Chemistry
Georg August University Göttingen
Tammannstr. 6

37077 Göttingen
Germany

phone: +49-551-201 10633
fax: +49-551-201 14411
e-mail: ajansho@gwdg.de

Further Information

http://www.uni-goettingen.de/en/208570.html

Andreas Janshoff

- 1987 – 1989 Studies of Biology at the University of Münster
- 1989 – 1994 Studies of Chemistry at the University of Münster, with honor
- 1994 – 1997 PhD thesis under supervision of Prof. Dr. H.-J. Galla
- 1997 – 1998 Postdoctoral Researcher at the Scripps Research Institute (La Jolla, CA, USA)
- 1999 – 2001 Habilitation in Biochemistry at the University of Münster in the group of Prof. Dr. H.-J. Galla and Prof. Dr. H. Fuchs
- 2001 – 2006 Associate Professor (C3) for Physical Chemistry at the University of Mainz
- 2006 – 2008 Full Professor (W3) for Biophysical Chemistry at the University of Mainz
- since 2008 Full Professor (W3) for Biophysical Chemistry at the University of Göttingen

Major Research Interests

- Membrane Biophysics
- Cell mechanics
- Sensor design
- Single-molecule force spectroscopy

Selected Recent Publications

Stephan M, Mey I, Steinem C, Janshoff A (2014) Combining reflectometry and fluorescence microscopy: An assay for the investigation of leakage processes across lipid membranes. Anal Chem 86: 1366-1371

Rother J, Nöding H, Mey I, Janshoff A (2014) AFM-based microrheology reveals significant differences in the viscoelastic response between malign and benign cell lines. Open Biol 4: 140046

Aggarwal S, Snaidero N, Pähler G, Frey S, Sánchez P, Zweckstetter M, Janshoff A, Schneider A, Weil M-T, Schaap IAT, Görlich D, Simons M (2013) Myelin membrane assembly is driven by a phase transition of myelin basic proteins into a cohesive protein meshwork. PLOS Biol 11: e1001577

Bao C, Pähler G, Geil B, Janshoff A (2013) An optical fusion assay based on membrane coated spheres in a 2D assembly. J Am Chem Soc 135: 12176-12179

Bakhti M, Snaidero N, Schneider D, Aggarwal S, Möbius W, Janshoff A, Eckhardt M, Nave K-A, Simons M (2013) Loss of electrostatic cell-surface repulsion mediates myelin membrane adhesion and compaction in the central nervous system. Proc Natl Acad Sci USA 110: 3143-3148

Krick R, Busse R A, Scacioc A, Stephan M, Janshoff A, Thumm M, Kühnel K (2012) Structural and functional characterization of the two phosphoinositide binding sites of PROPPINs, a beta-propeller protein family. Proc Natl Acad Sci USA 109: E2042-E2049

Lorenz, B., Alvarez de Cienfuegos, L., Oelkers, M., Kriemen, E., Brand, C., Stephan, M., Sunnick, E., Yueksel, D., Kalsani, V., Kumar, K., Werz, D., Janshoff, A. (2012): A model system for cell adhesion mediated by weak carbohydrate-carbohydrate interactions. J Am Chem Soc 134: 3326-3329

Janke M, Rudzevich Y, Molokanova O, Metzroth T, Mey I, Diezemann G, Marszalek PE, Gauss J, Böhmer V, Janshoff A (2009) Mechanically locked nanocapsules under force allow reversible hydrogen bond breakage. Nat Nanotechnol 4: 225-229

Schuy S, Schäfer E, Yoder NC, Vogel R, Hobe S, Kumar K, Janshoff A (2009) Coiled coil lipopeptides mimicking the prehairpin intermediate of gp41. Angew Chemie Int Ed 48: 751-754

Address

Dept. of General, Visceral and Pediatric Surgery, University Medical Center Göttingen
Justus-von-Liebig-Weg 11

37077 Göttingen
Germany

phone: +49-551-39 13711
fax: +49-551-39 13713
e-mail: steven.johnsen@med.uni-goettingen.de

Further Information

http://www.epigenesys.eu/index.php/fr/about-us/associate-members/864-steven-a-johnsen

Steven Johnsen

Full Professor for Translational Cancer Research

- 1999 – 2002 Ph.D. Mayo Clinic College of Medicine, Rochester, Minnesota, USA
- 2003 – 2006 Doctoral Fellow, Center for Molecular Neurobiology (ZMNH), Hamburg, Germany
- 2006 – 2007 Post-Doctoral Fellow, European Molecular Biology Laboratory (EMBL), Heidelberg, Germany
- 2007 – 2012 Assistant Professor in Molecular Oncology, University of Göttingen Medical Faculty, Göttingen, Germany
- 2012 – 2014 Assoc. Professor in Tumor Biology, University Medical Center Hamburg-Eppendorf, Hamburg, Germany
- Since 2014 Professor for Translational Cancer Research, University Medical Center Göttingen, Göttingen, German

Major Research Interests

The 3 x 10^9 bp of DNA in the human genome is organized in several higher order chromatin structures which allow for the correct packaging and “reading” of the genetic material. Importantly, the proper regulation of gene transcription, DNA replication and probably most DNA-associated nuclear functions is regulated by the post-translational modification of histone proteins. Our group is focused on the role and regulation of chromatin modifications in controlling transcription and transcription-coupled nuclear processes during tumorigenesis. The primary interest of our work is the monoubiquitination of histone H2B (H2Bub1) which appears to serve a tumor suppressor role in breast cancer and is tightly associated to active gene transcription. Although this modification has been studied extensively in yeast, relatively little is known about its function and regulation in higher eukaryotic organisms.
In our future work we will address:

1. The role of H2B modifying enzymes in tumorigenesis in transgenic mouse models.
2. The regulation of tumorigenic properties and metastasis by epigenetic modifiers.
3. How epigenetic modifications control cellular differentiation and dedifferentiation.
4. The function of dynamics changes in chromatin structure in various nuclear processes including transcription and DNA repair.

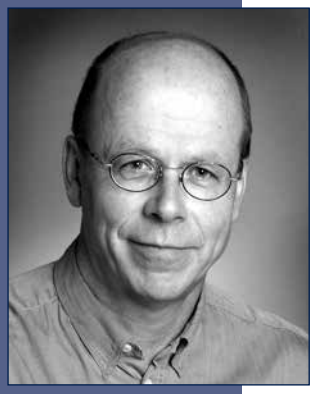
Selected Recent Publications

Nagarajan S, Benito E, Johnsen SA (2015) H4K12ac is regulated by estrogen receptor-alpha and is associated with BRD4 function and inducible transcription. Oncotarget 6(9): 7305-17

Bedi U, Scheel AH, Hennion M, Begus-Nahrmann Y, Ruschoff J, Johnsen SA (2015) SUPT6H controls estrogen receptor activity and cellular differentiationby multiple epigenomic mechanisms. Oncogene 34: 465-73

Nagarajan S, Hossan T, Alawi M, Najafova Z, Indenbirken D, Bedi U, Taipaleenmäki H, Ben-Batalla I, Scheller M, Loges S, Knapp S, Hesse E, Chiang CM, Grundhoff A, Johnsen SA (2014) romodomain protein BRD4 is required for estrogen receptor-dependent enhancer activation and gene transcription. Cell Reports 8(2): 460-9

Karpiuk O, Najafova Z, Kramer F, Hennion M, Galonska C, König A, Snaidero N, Vogel T, Shchebet A, Begus-Nahrmann Y, Kassem M, Simons M, Shcherbata H, Beissbarth T, Johnsen SA (2012) The histone H2B monoubiquitination regulatory pathway is required for differentiation of multipotent stem cells. Mol Cell 46(5): 705-13



Address

Developmental Biology
Research Group
Max Planck Institute
for Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 1560
fax: +49-551-201 1504
e-mail: mkessel1@gwdg.de

Further Information

http://www.mpibpc.mpg.de/de/kessel

Michael Kessel

Professor of Molecular Biology

- Until 1981 Biochemical Institute, Kiel University
- 1981 – 1983 National Cancer Institute, NIH, Bethesda,USA
- 1983 – 1986 Center for Molecular Biology (ZMBH), Heidelberg University
- Since 1987 Max Planck Institute for Biophysical Chemistry, Göttingen

Major Research Interests

The group is interested in the coordination between cell cycle and developmental control processes in mice. We apply biochemical, genetic and embryological techniques. We previously identified the Geminin protein as a mediator between cell cycle progression and the control of axial specification. Studying a conditional mouse knock-out model we found that Geminin is essential for the first cell divisions in murine embryos, but not later in development. Geminin is also necessary for the establishment, growth and maintenance of murine embryonic stem cells.

We further analyze the Mad2l2, a regulator of the APC/C complex, and a subunit of translesion DNA polymerase zeta and potential regulator of the cell cycle. We discovered an essential role of Mad2l2 for germ cell development during early embryogenesis, and during the generation of primordial germ cells from embryonic stem cells in culture. In the absence of Mad2l2 the pluripotency of embryonic stem cells becomes destabilized, and they differentiate into primitive endoderm.

Selected Recent Publications

Pirouz M, Rahjouei A, Shamsi F, Eckermann KN, Salinas-Riester G, Pommerenke C, Kessel M (2015). Destabilization of pluripotency in the absence of Mad2l2. Cell Cycle 14 (10): 1596-1610

Song R, Walentek P, Sponer N, Klimke A, Lee JS, Dixon G, Harland R, Wan Y, Lishko P, Lize M, Kessel M, He L (2014) miR-34/449 miRNAs promote motile ciliogenesis through direct regulation of Cp110 in multiciliated airway cells. Nature 510: 115-120

Pirouz M, Pilarski S, Kessel M (2013) A critical function of Mad2l2 in primordial germ cell development of mice. PLOS Genetics 9: 8, e1003712

Tabrizi GA, Böse K, Reimann Y, Kessel M (2013) Geminin is required for the maintenance of pluripotency. Plos One 8: 9, e73826

Asli NS, Kessel M (2010) Spatiotemporally restricted regulation of generic motor neuron programs by *miR-196*-mediated repression of Hoxb8. Dev Biol 344: 857-868

Luo L, Yang X, Takihara Y, Knoetgen H, Kessel M (2004) The cell-cycle regulator geminin inhibits Hox function through direct and polycomb-mediated interactions. Nature 427: 749-53

Address

Third Institute of Physics
Dept. of Biophysics
University of Göttingen
Friedrich-Hund-Platz 1

37077 Göttingen
Germany

phone: +49-551-39 13209
fax: +49-551-39 7720
email: dklopfe@gwdg.de

Further Information

http://www.uni-goettingen.de/de/arbeitsgruppen/507362.html

Dieter Klopfenstein

Junior Group Leader at the Centre for Molecular Physiology of the Brain, University of Göttingen

- Dr. phil. nat. (Ph.D.) University of Basel, 1999
- Postdoctoral fellow at the University of California San Francisco, 1999 – 2003
- Since 2003 head of an independent Junior Research Group

Major Research Interests

The long-range transport of membrane organelles in neurons depends primarily upon microtubules and motor proteins that move unidirectionally along these tracks. One type of microtubule-based motor proteins powering membrane transport is the kinesin superfamily. We are interested in how these motors achieve specificity in cargo binding, elicit membrane transport, and the regulation of transport activity. In addition, the fascinating organization of the muscle's sarcomere guides our research in understanding the orchestration of individual constituents in muscle contraction. Using fluorescently tagged motor and vesicle markers we investigate these questions in the nervous system of the nematode *C. elegans* serves us as a model system for microscopic tools (confocal, TIRF, FRET FLIM) and biochemical transport assays *in vitro*.

Selected Recent Publications

Butkevich E, Bodensiek K, Fakhri N, von Roden K, Schaap IA, Majoul I, Schmidt CF, Klopfenstein DR (2015) Drebrin-like protein DBN-1 is a sarcomere component that stabilizes actin filaments during muscle contraction. Nat Commun 6: 7523

Düselder A, Fridman V, Thiede C, Wiesbaum A, Goldstein A, Klopfenstein DR, Zaitseva O, Janson ME, Gheber L, Schmidt CF (2015) Deletion of the Tail Domain of the Kinesin-5 Cin8 Affects Its Directionality. J Biol Chem 290(27): 16841-50

Address

Dept of Molecular Genetics
University of Göttingen
Grisebachstr. 8

37077 Göttingen
Germany

phone: +49-551-39 9653
fax: +49-551-39 3805
email: wkramer@gwdg.de

Further Information

http://www.img.bio.uni-goettingen.de/molgen.htm

Wilfried Kramer

Privatdozent Molecular Biology and Genetics

- Diploma (Biology), University of Cologne, Germany, 1982
- Dr. rer. nat., University of Cologne, Germany, 1986
- Postdoctoral Fellow, University of California, Berkeley, USA, 1986 – 1989
- Habilitation in Molecular Biology and Genetics, University of Göttingen, Germany, 2000
- At the Dept. of Molecular Genetics since 1989

Major Research Interests

In the Department of Molecular Genetics, headed by Prof. Dr. H. Krebber, I try to identify new factors that might be involved in the export of mRNA from the nucleus in *Saccharomyces cerevisiae*. To this end, ordered mutants arrays are screened for genetic interactions with selected mutants by the so called SGA technique, which makes use of the genetic features offered by budding yeast to rapidly construct double mutants and compare their growth with that of single mutants. Furthermore, we want to extend these studies in different collaborations to microscopic screenings of those mutant arrays for export defects using automated microscopes. In a collaboration with Prof. Dr. S. Emmert from the medical faculty we want to analyse the function of the yeast *MPH1* gene and of its human homologue *FANCM*. The latter is a determining factor of the hereditary disease Fanconi anemia, which is – besides other symptoms - characterised by chromosome instability and increased incidence of cancer. Both are associated to homologous recombination and at least Mph1 is very likely involved in the error-free bypass of lesions, which are caused by DNA damaging agents and are blocking DNA replication, posing a very serious threat to the survival of the cell. Understanding these cellular responses to DNA damage will allow a better insight into central processes involved in the malignant transformation of cells.

Selected Recent Publications

Popova B, Schubert S, Bulla I, Buchwald D, Kramer W (2015) A Robust and Versatile Method of Combinatorial Chemical Synthesis of Gene Libraries via Hierarchical Assembly of Partially Randomized Modules. PLoS One 10(9):e0136778

Ede C, Rudolph CJ, Lehmann S, Schürer KA, Kramer W (2011) Budding yeast Mph1 promotes sister chromatid interactions by a mechanism involving strand invasion. DNA Repair 10: 45-55

Schomacher L, Schürer KA, Ciirdaeva E, McDermott P, Chong J, Kramer W, Fritz HJ (2010) Archaeal DNA uracil repair via direct strand incision: A minimal system reconstituted from purified components. DNA Repair 9: 438-447

Panico ER, Ede C, Schildmann M, Schürer KA, Kramer W (2010) Genetic evidence for a role of *Saccharomyces cerevisiae* Mph1 in recombinational repair under replicative stress. Yeast 27: 11-27

Prakash R, Satory D, Dray E, Papusha A, Scheller J, Kramer W, Krejci L, Klein H, Haber JE, Sung P, Ira G (2009) Yeast Mph1 helicase dissociates Rad51-made D-loops: implications for crossover control in mitotic recombination. Genes Dev 23: 67-79

Schürer KA, Rudolph C, Ulrich HD, Kramer W (2004) Yeast MPH1 gene functions in an error-free DNA damage bypass pathway that requires genes from homologous recombination, but not from postreplication repair. Genetics 166: 1673-1686

Address

Prof. Dr. Heike Krebber
Dept. of Molecular Genetics
Institute for Microbiology
and Genetics
University of Göttingen
Grisebachstr. 8

37077 Göttingen
Germany

Tel.: +49-551-39 33801
Fax: +49-551-39 33805
e-mail: heike.krebber@
biologie.uni-
goettingen.de

Further Information

http://www.img.bio.uni-goettingen.de/molgen.htm

Heike Krebber

Professor for Molecular Genetics

- 1996 Dr. rer. nat., Deutsches Krebsforschungszentrum, DKFZ, Heidelberg (Germany)
- 1996 Visiting Scientist, Weizman Institute of Science, Rehovot (Israel)
- 1996 – 1999 Scientist, Dana-Farber Cancer Institute, Harvard Medical School, Boston (USA)
- 1999 – 2010 Junior group leader, Institute for Molecular Biology and Tumor Research, Philipps-Universität Marburg (Germany)
- 2005 Habilitation in Molecular Biology
- 2006 Heisenberg Fellow
- since 2010 Professor for Molecular Genetics, Georg-August Universität Göttingen (Germany)

Major Research Interests

The compartimentation of eukaryotic cells requires a machinery that is able to transport a great number of molecules into and out of the nucleus in a rapid, accurate and regulated manner. The natural cargos for this machinery are proteins and RNA-protein complexes (RNPs). For the mRNPs it has to be assured that intron containing pre messenger RNAs are retained in the nucleus until proces-sing is completed. Only fully processed and spliced mRNAs are transported into the cytoplasm and translated at the ribosomes. The otherwise resulting gene products can be toxic to cells and harmful to organisms. Several examples exist where not fully processed pre-mRNAs reach the cytoplasm, resulting in di-seases like cancer or neurodegenerative diseases. Our projects aim to identify and characterize the requirements for mRNA processing, transport and translation. We want to learn which proteins are associated with the transported RNP, how transport is regulated and how the cell distinguishes between export incompetent and export competent mRNPs. Additionally, we study the maturation and functions of non-coding RNAs in eukaryotic cells. A major focus of both, coding and non-coding RNAs is their surveillance and quality control that prevent defects in cells. *Saccharomyces cerevisiae* has been proven to be a useful model organism for eukaryotic cells and we use a combination of genetics, biochemistry and cell biology to uncover these processes.

Selected Recent Publications

Wu H, Becker D, Krebber H (2014) Telomerase RNA TLC1 shuttling to the cytoplasm requires mRNA export factors and is important for telomere maintenance. Cell Rep 8: 1-9

Hackmann A, Wu H, Schneider UM, Meyer K, Jung K, Krebber H (2014) Quality control of spliced mRNAs requires the shuttling SR proteins Gbp2 and Hrb1. Nat Commun 5: 3123

Baierlein C, Hackmann A, Gross T, Henker L, Hinz F, Krebber H (2013) Monosome formation during translation initiation requires the serine/arginine-rich protein Npl3. Mol Cell Biol 33(24): 4811-23

Tieg B, Krebber H (2013) Dbp5 – From nuclear export to translation. Biochem Biophys Acta 1829: 791-798

Hackmann A, Gross T, Baierlein C, Krebber H (2011) The mRNA export factor Npl3 mediates the nuclear export of large ribosomal subunits. EMBO Rep 12(10): 1024-31

Baierlein C, Krebber H (2010) Translation termination: New factors and insights. RNA-Biology 7(5): 548-550

Khoshnevis S, Gross T, Rotte C, Baierlein C, Ficner R, Krebber H (2010) The iron-sulfur protein Rli1 functions in translation termination. EMBO Rep 11: 214-219

Gross T, Siepmann A, Sturm D, Windgassen M, Scarelli J, Cole CN, Seedorf M, Krebber H (2007) The DEAD box RNA helicase Dbp5 functions in translation termination. Science 315(5812): 646-649

Address

Dept. of Plant Cell Biology
Department of Plant Cell Biology
Schwann-Schleiden Research Center
University of Göttingen
Julia-Lermontowa-Weg 3

37077 Göttingen
Germany

phone: +49-551-39 177801
email: Volker.Lipka@biologie.uni-goettingen.de

Further Information

http://www.uni-goettingen.de/en/33181.html

Volker Lipka

Professor of Plant Cell Biology

- Dr. rer.nat. at the Department for Plant Molecular Biology, Technical University Aachen, 1999
- Postdoctoral fellow at the SainsburyLaboratory, John Innes Centre, Norwich, UK, 1999 – 2000
- Postdoctoral fellow at the Max-Planck Institute for Plant Breeding Research, Cologne, 2000 – 2004
- Leader of an independent research group at the Department for Plant Biochemistry, Centre for Plant Molecular Biology, University of Tübingen, 2004 – 2007
- Leader of an independent research group at the Sainsbury Laboratory, John Innes Centre, Norwich, UK, 2007 – 2009
- Professor at the University of Göttingen since 2009

Major Research Interests

Our laboratory is interested in the molecular analysis of plant innate immunity. Our research is focused on 1) the molecular dissection of mechanisms that control activation of basal defence in the plant model *Arabidopsis thaliana* 2) the analysis of defence mechanisms that contribute to resistance against fungal pathogens 3) the identification of fungal effector molecules that interfere with the plant defence machinery and allow host plant colonization
In nature, plants are constantly exposed to above- and below-ground attack by a vast array of potential pathogens. However, most plants are immune to the majority of would-be pathogens and susceptible to only a relatively small number of adapted microbes. Using a novel plant-fungus interaction model system we recently identified several molecular components that are required for the activation (Gimenez-Ibanez et al., 2009) and execution of basal plant defence (Collins et al., 2003; Lipka et al., 2005; Stein et al., 2006; Kwon et al., 2008; Lipka et al., 2008). As a consequence, receptor-mediated recognition, pathogen-induced intracellular transport processes, dynamic organelle translocation and cytoskeletal rearrangements represent major research topics in our department. Suppression of these defence mechanisms is a key requirement for adapted pathogens and we recently began studies to identify secreted fungal effector molecules that are likely to be involved. We combine genetic, cell, molecular and biochemical experimental strategies to gain novel insights into these complex mechanisms.

Selected Recent Publications

Willmann R, Lajunen HM, Erbs G, Newman MA, Kolb D, Tsuda K, Katagiri F, Fliegmann J, Bono JJ, Cullimore JV, Jehle AK, Götz F, Kulik A, Molinaro A, Lipka V, Gust AA, Nürnberger T (2011) *Arabidopsis* lysin-motif proteins LYM1 LYM3 CERK1 mediate bacterial peptidoglycan sensing and immunity to bacterial infection. Proc Nat Acad Sci USA 108(49): 19824-19829

Petutschnig EK, Jones AM, Serazetdinova L, Lipka U, Lipka V (2010) The Lysin Motif Receptor-like Kinase (LysM-RLK) CERK1 is a major chitin-binding protein in *Arabidopsis thaliana* and subject to chitin-induced phosphorylation. J Biol Chem 285(37): 28902-28911

Gimenez-Ibanez S, Hann DR, Ntoukakis V, Petutschnig E, Lipka V*, Rathjen JP* (2009) AvrPtoB targets the LysM receptor kinase CERK1 to promote bacterial virulence on plants. Curr Biol 19: 423-429, *co-corresponding authors

Kwon C, Neu C, Pajonk S, Yun HS, Lipka U, Humphry ME, Bau S, Straus M, Rampelt H, El Kasmi F, Jürgens G, Parker J, Panstruga R*, Lipka V*, Schulze-Lefert P* (2008) Co-option of a default secretory pathway for plant immune responses. Nature 451: 835-840, *co-corresponding authors

Lipka V, Dittgen J, Bednarek P, Bhat RA, Stein M, Landtag J, Brandt W, Scheel D, Llorente F, Molina A, Wiermer M, Parker J, Somerville SC, Schulze-Lefert P (2005) Pre- and post-invasion defenses both contribute to non-host resistance in *Arabidopsis*. Science 310: 1180-1183

Address

Dept. Cellular Biochemistry
Max Planck Institute for
Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 1407
fax: +49-551-201 1197
e-mail: reinhard.luehrmann
@mpi-bpc.mpg.de

Further Information

http://www.mpibpc.gwdg.de/research/dep/luehrmann/

Reinhard Lührmann

Professor, Director at the Max Planck Institute for Biophysical Chemistry

- Dr. rer. nat (Ph. D.), University of Münster (1975)
- Research group leader, Max Planck Institute for Molecular Genetics, Berlin (1981 – 1988)
- Professor of Biochemistry and Molecular Biology at the University of Marburg (1988 – 1999)
- Director, Dept. of Cellular Biochemistry, Max Planck Institute for Biophysical Chemistry, Göttingen (since 1999)
- Honorary Professor at the Georg August University of Göttingen

Major Research Interests

Most metazoan pre-mRNAs contain multiple introns and exons. In order to generate mature mRNA, the introns must be excised from the pre-mRNA, a process termed pre-mRNA splicing. In many cases, alternative splicing generates different mRNAs from a single pre-mRNA by the regulated removal of different sections of the RNA, a process which greatly expands the complexity of the repertoire of proteins that can be expressed from relatively small genomes. Splicing is catalysed by a large macromolecular machine, termed the spliceosome which consists of the small nuclear RNAs (U1, U2, U4, U5 and U6) and more than 150 proteins, 50 of which are associated with the snRNAs to form snRNPs.
In our laboratory, intense efforts are focussed on understanding how the spliceosome recognizes and binds the intron ends and discriminates them from exons. This is an especially confounding problem in metazoans because, in contrast to lower eucaryotes such as yeast, pre-mRNA introns are often extremely long (104-105 nucleotides), while exons are generally small (less than 300 nucleotides). Another major goal of our research is the elucidation of the mechanisms by which the spliceosome assembles into a catalytically active machine and catalyses intron excision. None of the building blocks of the spliceosome contains an active site. Instead, the catalytically active domain must be assembled anew on to each intron, a highly dynamic process which entails dramatic structural rearrangements of the RNP structure of the spliceosome, and which is orchestrated by the successive action of more than 10 enzymes such as RNA helicases and GTPases, as well as by posttranslational phosphorylation of a multitude of spliceosomal proteins. Our studies involve a large number of experimental approaches, including biochemical purification of entire spliceosomes or large protein ensembles, and characterization of their proteins by mass spectrometry; RNA biology methods such as enzymatic engineering of RNA molecules, RNA structure probing and RNA interference methods; production of recombinant proteins and antibodies; procedures for the investigation of protein-protein and protein-RNA interactions *in vitro* and *in vivo*; and biophysical methods such as fluorescence spectroscopy.
Finally, we are investigating the 3D structure of purified spliceosomes or major building blocks thereof using electron microscopic approaches and X ray crystallography. Our studies on the regulatory mechanisms of constitutive and alternative pre-mRNA splicing involve mainly mammalian systems. As the basic mechanisms of splicing catalysis appear to be evolutionarily highly conserved, we are also taking advantage of molecular genetic approaches in baker yeast to elucidate the structure and function of the catalytic core domain of the spliceosome.

Selected Recent Publications

Mozaffari-Jovin S, Wandersleben T, Santos KF, Will CL, Lührmann R, Wahl MC (2013) Inhibition of RNA helicase Brr2 by the C-terminal tail of the spliceosomal protein Prp8. Science 341: 80-84

Anokhina M, Bessonov S, Westhof E, Hartmuth K, Lührmann R (2013) RNA structure analysis in human spliceosomes reveals a compact 3D arrangement of snRNAs at the catalytic core. EMBO J 32: 2804-2818

Golas MM, Sander B, Bessonov S, Grote M, Wolf E, Kastner B, Stark H, Lührmann R (2010) 3D Cryo-EM structure of an active stepI spliceosome and localization of its catalytic core. Mol Cell 40: 927-938

Golas MM, Sander B, Bessonov S, Grote M, Wolf E, Kastner B, Stark H, Lührmann R (2010) 3D Cryo-EM structure of an active step 1 spliceosome and localization of its catalytic core. Mol Cell 40: 927-938

Wahl MC, Will CL, Lührmann R (2009) The spliceosome: design principles of a dynamic RNP machine. Cell 136: 701-718

Warkocki Z, Odenwälder P, Schmitzova J, Platzmann F, Stark H, Urlaub H, Ficner R, Fabrizio P, Lührmann R (2009) Reconstitution of both steps of *S. cerevisiae* splicing with purified spliceosomal components. Nature Struct Mol Biol 16: 1237-1243

Address

Dept. of Molecular
Cell Biology
Molecular Cell
Differentiation
Max Planck Institute for
Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 1709
fax: +49-551-201 1504
e-mail: amansou@gwdg.de

Further Information

http://www.mpibpc.mpg.de/groups/gruss

Ahmed Mansouri

Molecular Developmental Genetics

- Diploma (Chemistry), Technical University, Braunschweig (Germany) 1975
- Dr. rer. nat. Chemical Technology Institute, Technical University, Braunschweig (Germany), 1978
- Postdoc at the Institute of Human Genetics in Göttingen (1982 – 1986)
- Postdoc at the Miescher Institute in Tübingen (MPI) and at the Max Planck
- Institute of Immunbiology in Freiburg (Germany) (1986 – 1989)
- Since 1989 Dept of Molecular Cell Biology at the MPI for Biophysical Chemistry in Göttingen
- Habilitation (Molecular Developmental Genetics), University of Göttingen, Germany, 1999
- Since 2005: Dr. Helmut Storz Stiftungsprofessur for “dopaminerge Stammzelltherapie”, Dept. of Clinical Neurophysiology at the University of Göttingen

Major Research Interests

Studying the molecular mechanisms controlling cell fate destiny and diversity is of fundamental interest for understanding pathological processes and diseases. We are using mouse genetics to study the role of transcription factors during cell differentiation in the endocrine pancreas and in the ventral midbrain.

In the pancreas, we are interested in molecules that control the endocrine cell subtype specification. In addition, we are studying animal models to uncover molecular pathways promoting beta-cell regeneration in the adult pancreas.

In the midbrain the specification of dopaminergic neurons is under the control of several transcription and secreted factors. Specifically, we want to identify factors that interact with Lmx1 a/b in order to promote the generation of functionally distinct dopaminergic neuron populations.

Selected Recent Publications

Liao MC, Diaconu M, Monecke S, Collombat P, Timaeus C, Kuhlmann T, Paulus W, Trenkwalder C, Dressel R, Mansouri A (2014) Embryonic stem cell-derived neural progenitors as non-tumorigenic source for dopaminergic neurons. World Journal of Stem Cells 6(2): 248-255

Shamsi F, Parlato R, Collombat P, Mansouri A (2014) A genetic mouse model for progressive ablation and regeneration of insulin producing beta-cells. Cell Cycle 13(24): 3948-3957

Al-Hasani K, Pfeifer, A, Courtney M, Ben-Othman N, Gjernes E, Vieira A, Druelle N, Avolio F, Ravassard P, Leuckx G et al. (2013) Adult duct-lining cells can reprogram intoβ-like cells able to counter repeated cycles of toxin-induced diabetes. Developmental Cell 26 (1): 86-100

Courtney M, Gjernes E, Druelle N, Ravaud C, Vieira A, Ben-Othman N, Pfeifer A, Avolio F, Leuckx G, Lacas-Gervais S et al. (2013) The inactivation of Arx in pancreatic alpha-cells triggers their neogenesis and conversion into functional beta-like cells. PLoS Genetics 9 (10) (online published)

Address

Dept. of Bioinformatics
University of Göttingen
Goldschmidtstrasse 1

37077 Göttingen
Germany

phone: +49-551-39 14628
fax: +49-551-39 14966
e-mail: bmorgen@gwdg.de

Further Information

http://www.gobics.de/burkhard/

Burkhard Morgenstern

Professor of Bioinformatics

- 1993 Diploma (Mathematics), LMU München
- 1996 PhD (Dr. Math.), Universität Bielefeld
- 1997 – 1998 Visiting Scientist, North Carolina State University, Raleigh, NC, USA
- 1998 – 2000 RPR/Aventis, Dagenham, Essex, UK
- 2000 – 2001 MIPS, MPI fuer Biochemie, Martinsried and GSF, Neuherberg
- 2001 – 2002 Group leader and faculty member at International Graduate
- School in Bioinformatics and Genome Research, Univertität Bielefeld
- Since 2002 Professor of Bioinformatics, Universität Göttingen

Major Research Interests

The focus of our research work is algorithm and software development for nucleic acid and protein sequence analysis; the multiple-alignment program “DIALIGN” and the gene-finding program “AUGUSTUS” are widely used tools that have been developed in our department. More recently, we started to work on alignment-free approaches to comparative sequence analysis, here we developed the tools “kmacs” and “spaced words”.

Other areas of research in our department include: metabolomics and mass, spectroscopy data analysis, phylogeny reconstruction, metagenomics, motif discovery and remote homology detection using machine learning methods, genome annotation for prokaryotes, recombinations in viral genomes and HIV classification using coalescent theory.

Selected Recent Publications

Morgenstern B, B Zhu B, Horwege S, Leimeister C-A (2015) Estimating evolutionary distances between genomic sequences from spaced-word matches. Algorithms for Molecular Biology 10: 5

Kaever A, Landesfeind M, Feussner K, Mosblech A, Heilmann I, Morgenstern B, Feussner I, Meinicke P (2015) MarVis-Pathway: integrative and exploratory pathway analysis of non-targeted metabolomics data. Metabolomics 11: 764-777

Leimeister C-A, Morgenstern B (2014) kmacs: the k-Mismatch Average Common Substring Approach to alignment-free sequence comparison. Bioinformatics 30: 2000-2008

Leimeister C-A, Boden M, Horwege S, Lindner S, Morgenstern B (2014) Fast alignment-free sequence comparison using spaced-word frequencies. Bioinformatics 30: 1991-1999

Al Ait L, Yamak Z, Morgenstern B (2013) DIALIGN at GOBICS - multiple sequence alignment using various sources of external information. Nucleic Acids Res 41: W3-W7

Schultz A-K, Bulla I, Abdou-Chekaraou M, Gordien E, Morgenstern B, Zoulim F, Dény P, Stanke M (2012) jpHMM: Recombination analysis in viruses with circular genomes such as the hepatitis B virus. Nuc Acids Res 40: W193-W198

Address

Institute for Auditory Neuroscience
University Medical Center Göttingen
Robert-Koch-Str. 40

37075 Göttingen
Germany

phone: +49-551-39 22803
fax: +49-551-39 22299
e-mail: tmoser@gwdg.de

Further Information

http://www.auditory-neuroscience.uni-goettingen.de/

http://www.innerearlab.uni-goettingen.de/

https://www.mpibpc.mpg.de/14722384/moser

http://www.dpz.eu/en/platforms/optogenetics/auditory-neuroscience.html

Tobias Moser

Professor of Auditory Neuroscience

- MD University of Jena, 1995
- Postdoct with E. Neher at the MPI for Biophysical Chemistry, 1994 – 1997
- Junior Group Leader at the at the MPI for Biophysical Chemistry, Göttingen 1997 – 2001
- Residency in Otolaryngology, University Medical Center Göttingen 1997 – 2002
- Group Leader at the Department of Otolaryngology, University Medical Center Göttingen since 2001
- Research Group Leader at MPI for Biophysical Chemistry, MPI for Experimental Medicine and German Primate Center, Göttingen since 2014
- Director, Institute for Auditory Neuroscience, University Medical Center Göttingen 2015

Major Research Interests

Auditory Neuroscience - Synaptic Physiology and Pathophysiology – Audiology and Neuroprosthetics

Our work focuses on the molecular physiology and pathophysiology of sound encoding at the hair cell ribbon synapse and its restoration. We have physiologically and morphologically characterized synapses of wild-type and mutant mice with defects in hair cell synaptic coding from the molecular to the systems level. This way we have contributed to the understanding of structure and function of the hair cell ribbon synapse and co-initiated the concept of auditory synaptopathy. Molecular dissection and detailed physiological characterization of ribbon synapse function employ a spectrum of molecular, biophysical, physiological, psychophysical and clinical approaches. Towards restoration of hearing we pursue the optogenetic stimulation of cochlea and gene replacement therapy.

Selected Recent Publications

Jung S, Maritzen T, Wichmann C, Jing Z, Neef A, Revelo NH, Al-Moyed H, Meese S, Wojcik SM, Panou I, Bulut H, Schu P, Ficner R, Reisinger E, Rizzoli SO, Neef J, Strenzke N, Haucke V, Moser T (2015) Disruption of adaptor protein 2μ (AP-2μ) in cochlear hair cells impairs vesicle reloading of synaptic release sites and hearing. EMBO J 34(21): 2686-702

Jung S, Oshima-Takago T, Chakrabarti R, Wong AB, Jing Z, Yamanbaeva G, Picher MM, Wojcik SM, Göttfert F, Predoehl F, Michel K, Hell SW, Schoch S, Strenzke N, Wichmann C, Moser T (2015) Rab3-interacting molecules 2βand 2β promote the abundance of voltage-gated CaV1.3 Ca^{2+} channels at hair cell active zones. Proc Natl Acad Sci USA 112(24): E3141-9

PangršiβT, Gabrielaitis M, Michanski S, Schwaller B, Wolf F, Strenzke N, Moser T (2015) EF-hand protein Ca^{2+} buffers regulate Ca2+ influx and exocytosis in sensory hair cells. Proc Natl Acad Sci USA 112(9): E1028-37

Chapochnikov NM, Takago H, Huang CH, PangršiβT, Khimich D, Neef J, Auge E, Göttfert F, Hell SW, Wichmann C, Wolf F, Moser T (2014) Uniquantal release through a dynamic fusion pore is a candidate mechanism of hair cell exocytosis. Neuron 83(6): 1389-403

Mendoza Schulz A, Jing Z, Sánchez Caro JM, Wetzel F, Dresbach T, Strenzke N, Wichmann C, Moser T (2014) Bassoon-disruption slows vesicle replenishment and induces homeostatic plasticity at a CNS synapse. EMBO J 33(5): 512-27

Wong AB, Rutherford MA, Gabrielaitis M, Pangrsic T, Göttfert F, Frank T, Michanski S, Hell S, Wolf F, Wichmann C, Moser T (2014) Developmental refinement of hair cell synapses tightens the coupling of Ca^{2+} influx to exocytosis. EMBO J 33(3): 247-64

Address

Dept. of Neurogenetics
Max Planck Institute for
Experimental Medicine
Hermann-Rein-Strasse 3

37075 Göttingen
Germany

phone: +49-551-38 99757
fax: +49-551-38 99758
email: nave@em.mpg.de

Further Information

http://www.em.mpg.de/index.php?id=34&no_cache=1

Klaus-Armin Nave

Professor of Molecular Biology, Director at the Max Planck Institute of Experimental Medicine

- 1987 PhD, University of California, San Diego
- 1987 – 1991 Postdoc, The Salk Institute, la Jolla, California
- 1991 Junior Group Leader, ZMBH, University of Heidelberg
- 1998 Professor of Molecular Biology (C4), ZMBH, University of Heidelberg
- 2000 Director, Department of Neurogenetics, Max Planck Institute for Experimental Medicine Göttingen and Professor of Biology, University of Heidelberg

Major Research Interests

We are interested in the mechanisms of neuron-glia interactions in the higher nervous system, and in the genes that are required for normal glial cell function. Here, transgenic and mutant mice have become important to study developmental processes as well as genetic diseases. For example, oligodendrocytes are glial cells highly specialized for enwrapping CNS axons with multiple layers of membranes, known to provide electrical insulation for rapid impulse propagation. We found that oligodendrocytes are also essential for maintaining the long-term integrity of myelinated axons, independent of the myelin function itself. The mechanisms by which oligodendrocytes support long-term axonal survival are still under investigation. The importance of glial cells as the “first line of neuroprotection”, however, is illustrated by several myelin-associated diseases in which axonal neurodegeneration contribute to progressive disability. These range in humans from peripheral neuropathies (CMT1) to spastic paraplegia (SPG2), and presumably multiple sclerosis (MS) and certain forms of psychiatric disorders. We are developing transgenic animal models for some of these diseases, in order to dissect the underlying disease mechanisms and, in the case of CMT1A, have used these models to design novel therapeutic strategies.
The glial “decision” to myelinate an axonal segment is partly controlled by the axon itself, but the signaling mechanism is not understood. We have found that axonal neuregulin-1 (NRG1) is the major determinant of myelination in the peripheral nervous system. We are now investigating NRG1 dysregulation also in CNS myelination, using quantifiable behavioural functions in mice. By combining genetics with enviromental risk factors for schizophrenia (in collaboration with H. Ehrenreich) we will explore the hypothesis that NRG1, a known human schizophrenia susceptibility gene, points to an important role of myelinating glia in some psychiatric disorders.

Selected Recent Publications

Tzvetanova ID, Nave KA (2014) Axons hooked to Schwann cell metabolism. Nat Neurosci 17(10): 1293-5

Stassart RM, Fledrich R, Velanac V, Brinkmann BG, Schwab MH, Meijer D, Sereda MW, Nave K-A (2013) A role for Schwann cell derived neuregulin-1 in remyelination. Nat Neurosci 16: 48-54

Saher G, Rudolphi F, Corthals K, Ruhwedel T, Schmidt KF, Löwel S, Dibaj P, Barrette B, Möbius W, Nave K-A (2012) Therapy of Pelizaeus-Merzbacher disease in mice by feeding a cholesterol-enriched diet. Nat Med 18: 1130-1135

Fünfschilling U, Supplie LM, Mahad D, Boretius S, Saab AS, Edgar J, Brinkmann BG, Kassmann CM, Tzvetanova ID, Möbius W, Diaz F, Meijer D, Suter U, Hamprecht B, Sereda MW, Moraes CT, Frahm J, Goebbels S, Nave K-A (2012). Glycolytic oligodendrocytes maintain myelin and long-term axonal integrity. Nature 485: 517-521

Dhaunchak AS, Colman DR, Nave K-A (2011) Misalignment of PLP/DM20 transmembrane domains determines protein misfolding in Pelizaeus-Merzbacher disease. J Neurosci 31: 14961-14971

Nave K-A (2010) Myelination and support of axonal integrity by glia. Nature 468: 244-252

Address

X-Ray Crystallography
Research Group
Max Planck Institute
for Biophysical Chemistry

Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 1046
fax: +49-551-201 1197
e-mail: vpena@gwdg.de

Further Information

http://www.mpibpc.mpg.de/home/pena/

Vladimir Pena

Research Group Leader at the MPI for Biophysical Chemistry

- since 2014: Research group leader at the Max Planck Institute for Biophysical Chemistry, Goettingen, Germany
- 2009-2014: Project group leader at the Max Planck Institute for Biophysical Chemistry, Goettingen, Germany
- 2006-2008: Postdoctoral fellow at the Max Planck Institute for Biophysical Chemistry, Goettingen, Germany
- 2001-2005: PhD at the European Molecular Biology Laboratory (EMBL), Heidelberg, Germany
- 1995-2000: University of Bucharest, Romania

Major Research Interests

Pre-mRNA splicing is the essential step of gene expression in eukaryotes by which the non-coding regions are removed and the coding regions (exons) are ligated, resulting in the mature mRNA, ready for translation. The chemical basis of this process consists of two transesterification steps which are catalysed within the spliceosome, a multi-megadalton RNA-protein (ribonucleoprotein) machinery. Composed of an intricate RNA-RNA network and more than 50 conserved proteins, the spliceosome is assembled in a stepwise manner on the pre-mRNA substrate. The aim of our research group is to understand the structural basis of spliceosomal assembly, remodelling and catalysis at atomic level. Our main tool of investigation is X-ray crystallography, often complemented by biochemical, biophysical and genetic methods.

Selected Recent Publications

De I, Bessonov S, Hofele R, dos Santos K, Will CL, Urlaub H, Lührmann R, Pena V (2015) The RNA helicase Aquarius exhibits structural adaptations mediating its recruitment to spliceosomes. Nat Struct Mol Biol 22(2): 138-44

Hegele A, Kamburov A, Grossmann A, Sourlis C, Wowro S, Weimann M, Will CL, Pena V, Luhrmann R, Stelzl U (2012) Dynamic protein-protein interaction wiring of the human spliceosome. Mol Cell 45: 567-580

Schmitzova J, Rasche N, Dybkov O, Kramer K, Fabrizio P, Urlaub H, Luhrmann R, Pena V (2012) Crystal structure of Cwc2 reveals a novel architecture of a multipartite RNA-binding protein. Embo J 31(9): 2222-34

Hegele A, Kamburov A, Grossmann A, Sourlis C, Wowro S, Weimann M, Will CL, Pena V, Luhrmann R, Stelzl U (2012) Dynamic protein-protein interaction wiring of the human spliceosome. Mol Cell 45: 567-580

Pena V, Jovin SM, Fabrizio P, Orlowski J, Bujnicki JM, Luhrmann R, Wahl MC (2009) Common design principles in the spliceosomal RNA helicase Brr2 and in the Hel308 DNA helicase. Mol Cell 35: 454-466

Pena V, Rozov A, Fabrizio P, Luhrmann R, Wahl MC (2008b) Structure and function of an RNase H domain at the heart of the spliceosome. Embo J 27: 2929-2940

Pena V, Hothorn M, Eberth A, Kaschau N, Parret A, Gremer L, Bonneau F, Ahmadian MR, Scheffzek K (2008a) The C2 domain of SynGAP is essential for stimulation of the Rap GTPase reaction. EMBO Rep 9: 350-355

Pena V, Liu S, Bujnicki JM, Luhrmann R, Wahl MC (2007) Structure of a multipartite protein-protein interaction domain in splicing factor prp8 and its link to retinitis pigmentosa. Mol Cell 25: 615-624

Address

Dept. of Developmental Biochemistry
University Medical Center Göttingen
Justus-von-Liebig-Weg 11

37077 Göttingen
Germany

phone: +49-551-39 5683
+49-551-39 14613
fax: +49-551-39 14614
e-mail: tpieler@gwdg.de

Further Information

http://www.uni-bc.gwdg.de/entwickl/index.html

Tomas Pieler

Professor of Biochemistry

- Dr. rer. nat. Biochemistry, Freie Universität Berlin, 1984
- Guest Investigator, Rockefeller University, New York (1985/86)
- Heisenberg fellow, Freie Universität Berlin and Rockefeller University, New York (1986/87)
- Junior group leader, Max-Planck-Institut für Molekulare Genetik, Berlin (1988 – 1992)
- Professor of Biochemistry, Georg-August-Universität Göttingen (since 1992)
- Head of the Department of Developmental Biochemistry, Georg-August-Universität Göttingen

Major Research Interests

The differentiation of complex organisms has its origin in the asymmetric distribution of regulatory proteins or of the corresponding mRNAs in the egg, as well as in a complex system of cell/cell communication events via extracellular signalling molecules during early stages of embryogenesis. The genes that encode for these different activities form functional networks which provide the basis for the genetic programming of embryonic development. Our primary research interest is in the identification of such regulatory genes and networks in vertebrates, as well as in the definition of their regulation and function on the molecular level. For this purpose, we use *Xenopus laevis*, a frog from South Africa, as a model system. As a traditional object in experimental embryology and in comparison with other experimental systems such as the mouse, use of *Xenopus* offers a number of practical advantages. Oocytes and embryos are easy to collect in large numbers, they are easy to manipulate by relatively simple techniques, also because embryonic development proceeds in the petridish, and, more recently, it has even become possible to generate hundreds of transgenic frogs within a single experimental day. The research topics that we are focussing on are:

- Transport and function of vegetally localized maternal mRNAs
- Organogenesis: formation of pancreas and liver in vertebrate embryos
- Early neural development: primary neurogenesis
- Germ cell specification and migration

Selected Recent Publications

Claußen M, Lingner T, Pommerenke C, Opitz L, Salinas G, Pieler T (2015) Global analysis of asymmetric RNA enrichment in oocytes reveals low conservation between closely related *Xenopus* species. Mol Biol Cell 26(21): 3777-87

Bauermeister D, Claußen M, Pieler T (2015) A novel role for Celf1 in vegetal RNA localization during *Xenopus* oogenesis. Dev Biol 405(2): 214-24

Claußen M, Tarbashevich K, Pieler T (2011) Functional dissection of the RNA signal sequence responsible for vegetal localization of XGrip2.1 mRNA in *Xenopus* oocytes. RNA Biol 8(5): 873-82

Tarbashevich K, Dzementsei A, Pieler T (2011) A novel function for KiF13B in germ cell migration. Dev Biol 349: 169-178

Koebernick K, Löber J, Arthur P, Tarbashevich K, Pieler T (2010) Elr-type proteins protect *Xenopus* Dead end mRNA from miR-18-mediated clearance in the soma. Proc Nat Acad Sci 107: 16148-16153

Arthur PK, Claussen M, Koch S, Tarbashevich K, Jahn O, Pieler T (2009) Participation of *Xenopus* Elr-type proteins in vegetal mRNA localization during oogenesis. J Biol Chem 284(30): 19982-92

Address

Dept. of Genetics of Eukaryotic Microorganisms
Institute of Microbiology and Genetics
University of Göttingen
Grisebachstr.8

37077 Göttingen
Germany

phone: +49-551-39 13930
fax: +49-551-39 10123
e-mail: spoegge@gwdg.de

Stefanie Pöggeler

Professor of Genetics of Eukaryotic Microorganisms

- 1993 Dr. rer. nat., Ruhr-Universität Bochum
- 1993 – 1995 Research associate
- 1995 – 2001 Postdoctoral research fellow and group leader
- 1997 Visiting Scientist, Institut de Génétique et Microbiologie, Laboratory of Dr. D. Zickler, Université Paris-Sud, Orsay, France
- 2000 Habilitation (Botany), Ruhr-Universität Bochum
- 2001 – 2003 Associate Professor of Botany (stand-in), University of Münster
- 2003 – 2006 University lecturer (Hochschuldozentin) and group leader, Ruhr-Universität Bochum
- since 2006 Associate Professor of Genetics of Eukaryotic Microorganisms, Georg-August-Universität Göttingen

Major Research Interests

Fruiting-body development in filamentous ascomycetes
Fruiting-body development in filamentous ascomycetes is a complex cellular differentiation process that requires special environmental conditions and is controlled by many developmentally regulated genes. We are interested in the genes regulating this development process. We use the homothallic (self-fertile) ascomycete *Sordaria macrospora* as a model organism. Numerous mutants which are blocked at various stages of fruiting-body development have been generated and molecular genetic procedures have been applied to isolate genes involved in fruiting-body development. In addition to mutants generated by chemical mutagenesis, several mutants affecting fruiting-body development were produced by knock-out of mating-type genes, pheromone and receptor genes, as well as genes involved in autophagy and bicarbonate metabolism.

Autophagy in filamentous ascomycetes
Autophagy is defined as a tightly controlled non-selective degradation process in which eukaryotic cells digest their own proteins and organelles in response to starvation or stress conditions. In filamentous ascomycetes, autophagy is involved in various developmental processes. However, the exact role of autophagy in multicellular fruiting-body development is largely unknown.
Using a reverse genetics approach, we have recently shown that the autophagy genes *Smatg8* and other conserved genes required for core functions of the selective and non-selective autophagic machinery are essential for fruiting-body development in the filamentous ascomycete *Sordaria macrospora*. Our aim is to understand how selective autophagy contributes to vegetative growth and fruiting-body development in filamentous ascomycetes.

Selected Recent Publications

Frey S, Lahmann Y, Hartmann T, Seiler S, Pöggeler S (2015) Deletion of *Smgpi1* encoding a GPI-anchored protein suppresses sterility of the STRIPAK mutant ΔSmmob3 in the filamentous ascomycete *Sordaria macrospora*. Mol Microbiol 97: 676-697

Voigt O, Pöggeler S (2013) Autophagy genes Smatg8 and Smatg4 are required for fruiting-body development, vegetative growth and ascospore germination in the filamentous ascomycete *Sordaria macrospora*. Autophagy 9: 33-49

Bloemendal S, Bernhards Y, Bartho K, Dettmann A, Voigt O, Seiler S, Wolters DA, Pöggeler S, Kück U (2012) A homolog of the human STRIPAK complex controls sexual development in fungi. Mol Microbiol 84: 310-323

Klix V, Nowrousian M, Ringelberg C, Lorros JJ, Dunlap JC, Pöggeler S (2010) Functional characterization of MAT1-1-specific mating type genes in the homothallic ascomycete Sordaria macrospora provides new insights into essential and non-essential sexual regulators. Eukaryotic Cell 9: 894-905

Elleuche S, Pöggeler S (2009) β-Carbonic anhydrases play a role in fruiting body development and ascospore germination in the filamentous fungus *Sordaria macrospora*. PloS One 4:e5177

Storlazzi A, Tesse S, Ruprich-Robert G, Gargano S, Pöggeler S, Kleckner N, Zickler D (2008) Coupling meiotic chromosome axis integrity to recombination. Genes Dev 15: 796-809

Address

Infection Biology Unit
German Primate Center
Kellnerweg 4

37077 Göttingen
Germany

phone: +49-551-38 51150
fax: +49-551-39 51184
e-mail: s.poehlmann@dpz.eu

Further Information

http://www.dpz.eu/en/career/leibniz-graduate-schools/emerging-infectious-deseases.html

Stefan Pöhlmann

Professor, Head of the Infection Biology Unit, German Primate Center

- 2000: Ph.D., Friedrich-Alexander-University Erlangen-Nürnberg
- 2000 – 2003: Postdoctoral Fellow, University of Pennsylvania
- 2003 – 2007: Head of a SFB Junior Research Group, Institute of Clinical and Molecular Virology, Friedrich-Alexander-University Erlangen-Nürnberg
- 2007 – 2010: Professor for Experimental Virology, Hannover Medical School
- 2010: Professor and Head of the Infection Biology Unit of the German Primate Center

Major Research Interests

The Infection Biology Unit investigates virus host cell interactions with a focus on the first step of the infection process, viral entry into target cells.
Emerging viruses, like the Middle East Respiratory Syndrome (MERS) coronavirus, can pose a serious threat to public health. Activation by host cell proteases is essential for infectivity of many emerging viruses. We are elucidating which proteolytic systems are hijacked by emerging corona-, filo-, bunya- and influenza viruses for activation. On the basis of this information we will identify inhibitors and evaluate their antiviral activity in cell culture and animal models. Moreover, we are interested in defining which host cell receptors are used by emerging viruses for cellular entry. Finally, we are investigating how interferon-induced antiviral effector molecules inhibit infection by emerging viruses.
Human immunodeficiency virus (HIV) is the causative agent of the acquired immunodeficiency syndrome (AIDS), a major global health crisis. We seek to understand how the composition of the glycan coat of the HIV envelope protein modulates viral spread in and between individuals. This question will be addressed by employing simian immunodeficiency virus (SIV) infection of macaques as model system for HIV infection of human molecules of the innate immune system.

Selected Recent Publications

Zmora P, Moldenhauer AS, Hofmann-Winkler H, Pöhlmann S (2015) TMPRSS2 Isoform 1 Activates Respiratory Viruses and Is Expressed in Viral Target Cells. PLoS One 10(9): e0138380

Karsten CB, Buettner FF, Cajic S, Nehlmeier I, Neumann B, Klippert A, Sauermann U, Reichl U, Gerardy-Schahn R, Rapp E, Stahl-Hennig C, Pöhlmann S (2015) Exclusive Decoration of Simian Immunodeficiency Virus Env with High-Mannose Type N-Glycans Is Not Compatible with Mucosal Transmission in Rhesus Macaques. J Virol 89(22): 11727-33

Gnirß K, Zmora P, Blazejewska P, Winkler M, Lins A, Nehlmeier I, Gärtner S, Moldenhauer AS, Hofmann-Winkler H, Wolff T, Schindler M, Pöhlmann S. Tetherin (2015) Sensitivity of Influenza A Viruses Is Strain Specific: Role of Hemagglutinin and Neuraminidase. J Virol 89(18): 9178-88

Wrensch F, Winkler M, Pöhlmann S (2014) IFITM proteins inhibit entry driven by the MERS-coronavirus spike protein: evidence for cholesterol-independent mechanisms. Viruses 6(9): 3683-98

Gierer S, Müller MA, Heurich A, Ritz D, Springstein BL, Karsten CB, Schendzielorz A, Gnirß K, Drosten C, Pöhlmann S (2014) Inhibition of proprotein convertases abrogates processing of the middle eastern respiratory syndrome coronavirus spike protein in infected cells but does not reduce viral infectivity. J Infect Dis 211(6): 889-97

Kühl A, Münch J, Sauter D, Bertram S, Glowacka I, Steffen I, Specht A, Hofmann H, Schneider H, Behrens G, Pöhlmann S (2010) Calcium-modulating cyclophilin ligand does not restrict retrovirus release. Nat Med 16: 155-6

Address

Dept. of Cellular Biochemistry
University Medical Center Göttingen
Humboldtallee 23

37073 Göttingen
Germany

phone: +49-551-39 5947
fax: +49-551-39 5979
e-mail: peter.rehling@medizin.uni-goettingen.de

Further Information

http://www.uni-bc.gwdg.de/index.php

Peter Rehling

Professor, Director of the Dept. of Cellular Biochemistry

- 1996 Dr. rer. nat. (Biology), University of Bochum
- 1996 – 1998 Postdoctoral fellow (Laboratory of W.-H. Kunau, Bochum)
- 1998 – 2000 Postdoctoral fellow (S.D. Emr, HHMI, University of California San Diego, USA)
- 2000 – 2004 Research Group leader at the Institute for Biochemistry and Molecular Biology, Freiburg
- 2003 Habilitation (Biochemistry and Molecular Biology), University of Freiburg
- 2004 – 2007 Assistant Professor Institute for Biochemistry and Molecular Biology, Freiburg
- Since 2007 Professor of Biochemistry and Director of the Dept. of Biochemistry II University of Göttingen
- Since 2009 Speaker of the Study Section “Molecular Cell Biology” of the German Society for Biochemistry and Molecular Biology (GBM)
- Since 2010 Group associated with the Max Planck Institute for Biophysical Chemistry

Major Research Interests

We are interested in understanding the molecular mechanisms by which proteins are transported across the mitochondrial membranes and to find out how multi-protein complexes in the inner membrane (TIM complexes; translocation machineries of the inner membrane) mediate this task. In another aspect of our work we addresses the question how newly imported proteins assemble into multi-protein complexes in the inner membrane. In case of the respiratory chain complexes the assembly process is especially demanding since central subunits of the complexes are made within mitochondria. Dedicated chaperone- like factors are required to assist and regulate assembly and translation in mitochondria. The analysis of the principles of the biogenesis process and the activities of the assembly factors is of central importance for our understanding of the molecular basis of human mitochondrial disorders.

Selected Recent Publications

Melin J, Kilisch M, Neumann P, Lytovchenko O, Gomkale R, Schendzielorz A, Schmidt B, Liepold T, Ficner R, Jahn O, Rehling P, Schulz C (2015) A presequence-binding groove in Tom70 supports import of Mdl1 into mitochondria. Biochim Biophys Acta 1853(8): 1850-9

Schulz C, Rehling P (2014) Cell biology. Powering the cell cycle. Science 346(6213): 1059-60

Melin J, Schulz C, Wrobel L, Bernhard O, Chacinska A, Jahn O, Schmidt B, Rehling P (2014) Presequence recognition by the tom40 channel contributes to precursor translocation into the mitochondrial matrix. Mol Cell Biol 34(18): 3473-85

Lytovchenko O, Melin J, Schulz C, Kilisch M, Hutu DP, Rehling P (2013) Signal recognition initiates reorganization of the presequence translocase during protein import. EMBO J 32: 886-898

Mick DU, Dennerlein S, Wiese H, Reinhold R, Pacheu-Grau D, Lorenzi I, Sasarman F, Weraarpachai W, Shoubridge EA, Warscheid B, Rehling P (2012) MITRAC Links Mitochondrial Protein Translocation to Respiratory-Chain Assembly and Translational Regulation. Cell 151: 1528–1541

Vukotic M, Oeljeklaus S, Wiese S, Vögtle FN, Meisinger C, Meyer HE, Zieseniss A, Katschinski DM, Jans DC, Jakobs S, Warscheid B, Rehling P*, Deckers M (2012) Rcf1 mediates cytochrome oxidase assembly and respirasome formation, revealing heterogeneity of the enzyme complex. Cell Metab 7: 336-347 (*corresponding author)

Address

Dept. of Neuro- and
Sensory Physiology
University Medical Center
Göttingen
Grisebachstr. 5

37077 Göttingen
Germany

phone: +49-551-39 3630
fax: +49-551-39 12346
e-mail: srizzol@gwdg.de

Further Information

http://rizzoli-lab.de/

Silvio Rizzoli

Group Leader STED Microscopy of Synaptic Function

- 2000 – 2004 Research assistant with William Betz at the Dep. of Physiology and Biophysics, University of Colorado Health Sciences Center (USA)
- 08/2004 PhD degree (Physiology) awarded by the University of Colorado
- 2004 – 2007 Post doctoral fellow with Reinhard Jahn at the Neurobiology
- Department of the Max Planck Institute for Biophysical Chemistry in Göttingen (Germany)
- since 2007 Group Leader (STED Microscopy) at the European Neuroscience Institute Göttingen (ENI-G)

Major Research Interests

Conventional fluorescence microscopy is limited by the diffraction of light: fluorescent objects that are close together cannot be discerned. Stimulated emission depletion (STED) is a recent advancement in optical physics that breaks the diffraction barrier, allowing microscopes to obtain much clearer images. The diffraction barrier has been particularly problematic for imaging synaptic vesicles, which are among the smallest known organelles (30-50 nm in diameter). They are located in small areas in the synapses (about 1 micron in diameter). The group takes advantage of the increased imaging resolution provided by STED to investigate synaptic vesicle function, with an emphasis on synaptic vesicle recycling. Since STED microscopy also allows imaging of protein domains, the group aims at studying the patterning of protein domains in the synapse, in order to understand its molecular architecture.

Selected Recent Publications

Vreja IC, NikiβI, Göttfert F, Bates M, Kröhnert K, Outeiro TF, Hell SW, Lemke EA, Rizzoli SO (2015) Super-resolution Microscopy of Clickable Amino Acids Reveals the Effects of Fluorescent Protein Tagging on Protein Assemblies. ACS Nano [Epub ahead of print]

Vreja IC, Kabatas S, Saka SK, Kröhnert K, Höschen C, Opazo F, Diederichsen U, Rizzoli SO (2015) Secondary-ion mass spectrometry of genetically encoded targets. Angew Chem Int Ed Engl 54(19): 5784-8

Saka SK, Honigmann A, Eggeling C, Hell SW, Lang T, Rizzoli SO (2014) Multiprotein assemblies underlie the mesoscale organization of the plasma membrane. Nat Commun 5: 4509

Wilhelm BG, Mandad S, Truckenbrodt S, Kröhnert K, Schäfer C, Rammner B, Koo SJ, Claßen GA, Krauss M, Haucke V, Urlaub H, Rizzoli SO. Composition of isolated synaptic boutons reveals the amounts of vesicle trafficking proteins. Science 344(6187): 1023-8

Saka SK, Vogts A, Kröhnert K, Hillion F, Rizzoli SO, Wessels JT (2014) Correlated optical and isotopic nanoscopy. Nat Commun 5: 3664

Opazo F, Levy M, Byrom M, Schäfer C, Geisler C, Groemer TW, Ellington AD, Rizzoli SO (2012) Aptamers as potential tools for super-resolution microscopy. Nat Methods 9: 938-939

Denker A, Bethani I, Kröhnert K, Körber C, Horstmann H, Wilhelm BG, Barysch SV, Kuner T, Neher E, Rizzoli SO (2011a) A small pool of vesicles maintains synaptic activity *in vivo*. Proc Natl Acad Sci USA 108: 17177-17182

Denker A, Kröhnert K, Bückers J, Neher E, Rizzoli SO (2011b) The reserve pool of synaptic vesicles acts as a buffer for proteins involved in synaptic vesicle recycling. Proc Natl Acad Sci USA 108: 17183-17188

Wilhelm BG, Groemer TW, Rizzoli SO (2010) The same synaptic vesicles drive active and spontaneous release. Nat Neurosci 13: 1454-1456

Hoopmann P, Punge A, Barysch SV, Westphal V, Bückers J, Opazo F, Bethani I, Lauterbach MA, Hell SW, Rizzoli SO (2010) Endosomal sorting of readily releasable synaptic vesicles. Proc Natl Acad Sci USA 107: 19055-19060

Address

Dept. of Physical Biochemistry
Max Planck Institute for Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 2901
fax: +49-551-201 2905
e-mail: rodnina@mpibpc.mpg.de

Further Information

http://www.mpibpc.mpg.de/research/dep/rodnina/

Marina Rodnina

Professor of Biochemistry

- PhD, Institute of Molecular Biology and Genetics, Academy of Science Ukraine, Kiew, Ukraine, 1989
- Research Fellow of the Alexander von Humboldt Foundation, University of Witten, Germany, 1990 – 1992
- Research Fellow at the Institute of Molecular Biology, University of Witten/Herdecke, 1992 – 1998
- Associate Professor for Physical Biochemistry at the Institute of Molecular Biology, University of Witten/Herdecke, 1998 – 2000
- Full Professor, Head of the Institute of Physical Biochemistry, University of Witten/Herdecke, 2000 – 2008
- Director of Department of Physical Biochemistry, Max Planck Institute for Biophysical Chemistry, Göttingen, since 2008

Major Research Interests

1. Ribosome function and dynamics
2. Regulation and fidelity of translation
3. Ribosome-catalyzed reactions

Protein synthesis from amino acids in the cell is performed on ribosomes, large ribonucleoprotein particles that consist of several RNA molecules and over 50 proteins, augmented by auxiliary translation factors. One important unresolved question is the relation between the speed and fidelity of protein synthesis, which are two fundamental parameters that define viability and fitness of cells. While normal decoding is very accurate, is special cases the ribosome can overcome the rules of normal translation to recode parts of the genome in an alternative way. Incorporation of unusual amino acids, such as selenocysteine, requires highly specialized machinery for delivery. Understanding the the movement of tRNAs and mRNA through the ribosome remains a major challenge. Finally, the processivity of the ribosome on the mRNA track, discontinuous translation and vectorial co-translational protein folding are open challenging questions. We investigate translation using a combination of techniques from Biochemistry, Structural Biology and Physical Biochemistry. Development of highly efficient and controlled ribosome translation systems on a highly sophisticated technological level is important for production of proteins with desired properties for purposes of proteomics and high-throughput structural studies emerging in the post-genomic era. The translational apparatus is a major target for antibiotics. Better understanding of the mechanisms of antibiotic action, resistance mechanisms and the interplay between resistance and bacterial fitness will be increasingly important for developing new antimicrobials and combating the major infectious diseases.

Selected Recent Publications

Adio S, Senyushkina T, Peske F, Fischer N, Wintermeyer W, Rodnina MV (2015) Fluctuations between multiple EF-G-induced chimeric tRNA states during translocation on the ribosome. Nat Commun 6: 7442

Caliskan N, Katunin VI, Belardinelli R, Peske F, Rodnina MV (2014) Programmed –1frameshifting by kinetic partitioning during impeded translocation. Cell 157: 1619-1631

Samatova E, Konevega AL, Wills NM, Atkins JF, Rodnina MV (2014) High-efficiency translational bypassing of non-coding nucleotides specified by mRNA structure and nascent peptide. Nature Communications 5: 4459

Doerfel LK, Wohlgemuth I, Kothe C, Peske F, Urlaub H, Rodnina MV (2013) EF-P is essential for rapid synthesis of proteins containing consecutive proline residues. Science 339: 85-88

Mittelstaet J, Konevega AL, Rodnina MV (2013) A kinetic safety gate controlling the delivery of unnatural amino acids to the ribosome. J Am Chem Soc 135: 17031-17038

Melina Schuh

Director at the Max Planck Institute for Biophysical Chemistry

- 2004 Diploma in Biochemistry, University of Bayreuth, Germany
- 2004 – 2008 Ph.D. Student, Laboratory of Jan Ellenberg, EMBL Heidelberg, Germany
- 2008 Dr. rer. nat., University of Heidelberg and EMBL Heidelberg, Germany
- 2009 – 2010 Senior Investigator Scientist, MRC LMB, Cambridge, UK
- 2010 – 2014 Programme Leader Track, MRC LMB, Cambridge, UK
- 2014 – 2015 Programme Leader (Tenured), MRC LMB, Cambridge, UK
- since 2016 Director of the Department of Meiosis, MPI for Biophysical Chemistry, Göttingen, Germany

Major Research Interests

We study meiosis in mammalian oocytes, the progenitor cells of eggs. This topic is of great interest for fundamental research because meiosis is still much more poorly understood than mitosis, especially in mammals. It is also of direct medical relevance because defects in eggs are the leading cause of pregnancy loss and several congenital disorders such as Down's syndrome. Our main aim is to understand how defects at the interface between chromosomes and cytoskeletal structures lead to aneuploid eggs and pregnancy loss in mammals. To this end, we study how the meiotic spindle is organized, how it segregates the chromosomes and how the spindle interacts with actin to drive the meiotic divisions. To have a solid foundation for future research, we are also developing new tools to study meiosis in mammalian oocytes. For instance, we have been able to carry out the first high content screen for meiotic genes in mammals. We have also been able to establish methods that now allow us for the first time to study the causes of chromosome segregation errors directly in live human oocytes. This has opened an exciting new area of research in my laboratory that we plan to expand significantly in the future.

Selected Recent Publications

Pfender S*, Kuznetsov V*, Pasternak M*, Tischer T, Santhanam B, Schuh M (2015) Live imaging RNAi screen reveals genes essential for meiosis in mammalian oocytes. Nature doi: 10.1038/nature14568, *equal contribution

Holubcová Z, Blayney M, Elder K, Schuh M (2015) Error-prone chromosome-mediated spindle assembly favors chromosome segregation defects in human oocytes. Science 348: 1143-1147

Clift D, Schuh M (2015) A three-step MTOC fragmentation mechanism facilitates bipolar spindle assembly in mouse oocytes. Nat Commun doi: 10.1038/ncomms8217

Clift D, Schuh M (2013) Restarting life: fertilization and the transition from meiosis to mitosis. Nat Rev Mol Cell Biol 14: 549-562

Holubcová Z, Howard G, Schuh M (2013) Vesicles modulate an actin network for asymmetric spindle positioning. Nat Cell Biol 15, 937-947

Schuh M (2011) An actin-dependent mechanism for long-range vesicle transport. Nat Cell Biol 13: 1431-1436

Address

Department of Meiosis
Max Planck Institute for Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

e-mail: melina.schuh@mpibpc.mpg.de

Further Information

http://www.mpibpc.mpg.de/mschuh

Address

Molecular Organogenesis
Research Group
Max Planck Institute for
Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 1758
fax: +49-551-201 1755
e-mail: rschuh@gwdg.de

Further Information

http://www.mpibpc.gwdg.de/abteilungen/170/schuh/

Reinhard Schuh

Research Group Leader at the MPI for Biophysical Chemistry

- Dr. rer. nat., University of Tübingen, Germany, 1986
- Postdoctoral Fellow at the Max Planck Institute for Developmental Biology, Tübingen, Germany, 1986 – 1988
- Postdoctoral Fellow at the University of Munich, Germany, 1989 – 1991
- Group leader in the Department of Molecular Developmental Biology at the Max Planck Institute for Biophysical Chemistry, Göttingen, Germany, 1992 – 2004
- Habilitation in Cellular and Molecular Biology, Technical University of Braunschweig, Germany, 2001
- Leader of the Research Group Molecular Organogenesis at the Max Planck Institute for Biophysical Chemistry, since 2005
- since 2008: Teaching as an adjunct professor on the Faculty of Biology at the University of Göttingen

Major Research Interests

Branched tubular networks are a fundamental structural design of many organs including lung, vascular system and kidney. Critical for organ function, i.e. the transport of fluids or gases, is the proper size and diameter of the tubular branches as well as an elaborated network formation. How do these networks develop? How do the branches grow out, detect their fusion partners and interconnect? How are tube size and dia-meter controlled? How can the system respond to different physiological needs? How do epidermal sheets control the paracellular passage of solutes?

We investigate the development of the *Drosophila* tracheal (respiratory) system since it provides an ideal model to address such questions, because of its simple stereotypic architecture, accessible genetics and molecular tools.

Selected Recent Publications

Hildebrandt A, Pflanz R, Behr M, Tarp T, Riedel D, Schuh R (2015) Bark beetle controls epithelial morphogenesis by septate junction maturation in *Drosophila*. Dev Biol 400(2): 237-47

Jaspers MH, Pflanz R, Riedel D, Kawelke S, Feussner I, Schuh R (2014) The fatty acyl-CoA reductase Waterproof mediates airway clearance in *Drosophila*. Dev Biol 385(1): 23-31

Jaspers MH, Nolde K, Behr M, Joo SH, Plessmann U, Nikolov M, Urlaub H, Schuh R (2012) The claudin Megatrachea protein complex. J Biol Chem 287(44): 36756-65

Weiss A, Charbonnier E, Ellertsdottir E, Tsirigos A, Wolf C, Schuh R, Pyrowolakis G, Affolter M (2010) A conserved activation element in BMP signaling during *Drosophila* development. Nature Struct Mol Biol 17: 69-76

Harder B, Schomburg A, Pflanz R, Küstner KM, Gerlach N, Schuh R (2008) TEV protease-mediated cleavage in *Drosophila* as a tool to analyze protein functions in living organisms. BioTechniques 44: 765-772

Krause C, Wolf C, Hemphälä J, Samakovlis C, Schuh R (2006) Distinct functions of the leucine-rich repeat transmembrane proteins Capricious and Tartan in the *Drosophila* tracheal morphogenesis. Dev Biol 296: 253-264

Adryan B, Schuh R (2004) Gene Ontology-based clustering of gene expression data. Bioinformatics 20: 2851-2852

Behr M, Riedel D, Schuh R (2003) The claudin-like Megatrachea is essential in septate junctions for the epithelial barrier function in *Drosophila*. Dev Cell 5: 611-620

Address

Dept. of Molecular Biology
University Medical Center
Göttingen
Humboldtallee 23

37073 Göttingen
Germany

Tel.: +49-551-39 5962
Fax: +49-551-39 5960
e-mail: blanche.schwappach@med.uni-goettingen.de

Further Information

http://www.uni-bc.gwdg.de/index.php?id=681

Blanche Schwappach

Professor, Director of Biochemistry I

- 1996 Dr rer nat (Biology), Centre for Molecular Neurobiology (ZMNH), University of Hamburg
- 1997 – 2000 Postdoctoral fellow (Laboratory of Lily Jan, University of California, San Francisco, USA)
- 2000 – 2007 Research group leader at the Centre for Molecular Biology (ZMBH), University of Heidelberg
- 2004 Habilitation (Molecular Biology and Cell Biology) at the ZMBH
- 2007 – 2010 Wellcome Trust Senior Research Fellow, Faculty of Life Sciences, University of Manchester, UK
- since 2010 Professor of Biochemistry and Director of the Department of Molecular Biology (former Biochemistry I)
- since 2010 the group is associated with the Max Planck Institute of Biophysical Chemistry

Major Research Interests

The group works on different aspects of membrane protein biogenesis and its integration into the physiology of organs such as the brain or the heart. We study the early life of tail-anchored proteins that are post-translationally targeted to the endoplasmic reticulum for membrane integration. Other projects address the role of sorting motifs during the passage of ion channels and neurotransmitter receptors through the secretory pathway. One channel under investigation (the KATP channel) couples cellular metabolism to insulin secretion in pancreatic beta cells. In the brain and the heart KATP channels play less defined roles that we currently address employing biochemical methods. We study biogenesis and trafficking under (patho)physiological conditions in genetically tractable model organisms such as yeast or mouse. Besides membrane protein biochemistry we use GFP-based physiological sensors for small molecules and ions in cellular compartments. This allows us to tackle how ion channels and transporters contribute to different physicochemical milieus inside cells.

Selected Recent Publications

Vilardi F, Stephan M, Clancy A, Janshoff A, Schwappach B (2014) WRB and CAML are necessary and sufficient to mediate tail-anchored protein targeting to the ER membrane. PLoS One 9(1): e85033

Arakel EC, Brandenburg S, Uchida K, Zhang H, Lin YW, Kohl T, Schrul B, Sulkin MS, Efimov IR, Nichols CG, Lehnart SE, Schwappach B (2014) Tuning the electrical properties of the heart by differential trafficking of KATP ion channel complexes. J Cell Sci 127(Pt 9): 2106-19

Wilhelm Voth, Markus Schick, Stephanie Gates, Sheng Li, Fabio Vilardi, Irina Gostimskaya, Daniel R. Southworth, Blanche Schwappach and Ursula Jakob (2014) The protein targeting factor GET3 functions as an ATP-independent chaperone under oxidative stress conditions. Molecular Cell 56: 116-127

Powis K, Schrul B, Tienson H, Gostimskaya I, Breker M, High S, Schuldiner S, Jakob U, Schwappach B (2013) Get3 is a holdase chaperone and moves to deposition sites for aggregated proteins when membrane targeting is blocked. J Cell Sci 126: 473-483

Braun NA, Morgan B, Dick TP, Schwappach B (2010) The yeast CLC protein counteracts vesicular acidification during iron starvation J Cell Sci 123: 2342-2350

Leznicki P, Clancy A, Schwappach B, High S (2010) Bat3 promotes the membrane integration of tail-anchored proteins. J Cell Sci 123: 2170-2178

Schuldiner M, Metz J, Schmid V, Denic V, Rakwalska M, Schmitt HD, Schwappach B, Weissman JS (2008) The GET Complex Mediates Insertion of Tail-Anchored Proteins into the ER. Cell 134: 635-645

Address

Gene Expression and
Signaling Group
Max Planck Institute for
Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 1656
fax: +49-551-201 1755
e-mail: halyna.shcherbata
@mpibpc.mpg.de

Further Information

http://www.mpibpc.mpg.de/research/ags/shcherbata/

Halyna Shcherbata

Max Planck Research Group Leader

- 1996 Ph.D., Genetics, Kyiv Institute for Plant Physiology and Genetics, Ukraine
- 1996 – 2003 Scientific Researcher, then Assistant Professor, Lemberg (Lviv) National University, Ukraine
- 2003 – 2008 Postdoc, then Research Professor, Biochemistry Department, Institute for Stem cell and Regenerative Medicine, University of Washington, Seattle, WA, USA
- 2008 – present Max Planck Research Group Leader, MPI for Biophysical Chemistry, Göttingen, Germany
- 2012 Habilitation in Developmental Biology, Georg-August University, Göttingen, Germany

Major Research Interests

My lab is focused on understanding of biological roles of miRNAs in cell differentiation and maintenance under normal, stress, and disease conditions in *Drosophila*. We show that the miRNAs-based regulatory network is accomplished via feedback-feedforward signaling, which allows to reduce transcriptional noise and fine-tune gene expression to regulate the entire gene expression profile. In addition, tissue-specific miRNAs direct differentiation toward corresponding lineages by suppressing alternative cell fates and ensuring the robustness of cell identity. Under stress and in chronic pathological states, miRNA levels are misregulated which disrupts tissue regeneration and homeostasis due to miRNA influence on cell proliferation and differentiation programs. We found that miRNAs act as spatio-temporal cell fate determinants, differentiation guardians and canalization factors, and stress response elements. We use *Drosophila* as a model organism that can serve as a valuable model system for conserved mechanisms underlying human disorders. One of our scientific interests is the analysis of the Dystrophin Glycoprotein Complex (DGC), perturbation in which results in muscular dystrophies and brain abnormalities in humans. We found that stress induces muscle degeneration even in wild type animals and accelerates age-dependent muscular dystrophy. In view of the facts that miRNAs have been implicated in stress response and the DGC has an effect on miRNA expression in vertebrates, we have conducted a miRNA microarray screen in stressed and not stressed wild type and dystrophic animals. The second line of the research that is actively conducted in my lab is focused on studying the role of the microRNA pathway in stem cells, where the *Drosophila* germline and neuronal stem cells are used as model systems. Our findings show that hormonal signaling and miRNAs direct neuronal and germline stem cell differentiation. Not only do steroid hormones control the miRNA expression, miRNAs also act in feedback loops to regulate the strength of the hormonal signaling. This provides the means to fine-tune the signals managing stem cell division, maintenance, and differentiation in response to ever-changing extracellular conditions.

Selected Recent Publications

König A, Shcherbata HR (2015) Soma influences GSC progeny differentiation via the cell adhesion-mediated steroid-let-7-Wingless signaling cascade that regulates chromatin dynamics. Biol Open 4(3): 285-300

Yatsenko AS, Marrone AK, Shcherbata HR. miRNA-based buffering of the cobblestone-lissencephaly-associated extracellular matrix receptor dystroglycan via its alternative 3'-UTR (2014) Nat Commun 5: 4906

Yatsenko AS, Shcherbata HR (2014) Drosophila miR-9a targets the ECM receptor Dystroglycan to canalize myotendinous junction formation. Dev Cell 28(3): 335-48

Kucherenko MM, Shcherbata HR (2013) Steroids as external temporal codes act via miRNAs and cooperate with cytokines in differential neurogenesis. Fly (Austin) 7: 3

Marrone AK, Edeleva EV, Kucherenko MM, Hsiao NH, Shcherbata HR (2012) Dg-Dys-Syn1 signaling in *Drosophila* regulates the microRNA profile. BMC Cell Biol 13: 26

Kucherenko MM, Barth J, Fiala A, Shcherbata HR (2012) Steroid-induced microRNA let-7 acts as a spatio-temporal code for neuronal cell fate in the developing *Drosophila* brain. EMBO J 31(24): 4511-23

König A, Yatsenko AS, Weiss M, Shcherbata HR (2011) Ecdysteroids affect *Drosophila* ovarian stem cell niche formation and early germline differentiation. EMBO J 30: 1549-1562

Kucherenko MM, Marrone AK, Rishko VM, Magliarelli Hde F, Shcherbata HR (2011) Stress and muscular dystrophy: a genetic screen for dystroglycan and dystrophin interactors in *Drosophila* identifies cellular stress response components. Dev Biol 352: 228-242

Address

Dept. of Structural Dynamics
Max Planck Institute for Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 1305
fax: +49-551-201 1197
e-mail: holger.stark@mpibpc.mpg.de

Further Information

http://www.mpibpc.mpg.de/groups/stark/

Holger Stark

Professor, Director at the Max Planck Institute for Biophysical Chemistry

- 1996 Dr. rer. nat. (Biochemistry) Free University of Berlin
- 1997 – 1998 Postdoc (Laboratory of Marin van Heel, Imperial College, London)
- 1998 – 1999 Junior group leader, University of Marburg
- 2000 – 2004 Junior group leader, MPI for Biophysical Chemistry
- 2005 – BioFuture group leader, MP for Biophysical Chemistry
- 2005 – 2007 BioFuture group leader
- since 2007 Professor for Molecular Electron Cryomicroscopy, University Göttingen and group leader, MPI for Biophysical Chemistry
- since 2015 Director, Dept. Structural Dynamics, MPI for Biophysical Chemistry

Major Research Interests

The work in our group is focused on 3D structure determination of large macromolecular complexes by single particle electron cryomicroscopy (cryo-EM). In cryo-EM, thousands of electron microscopical images of a macromolecular complex are taken at low temperature in the electron microscope and are used to calculate a 3D reconstruction of the object by computational image processing. Electron microscopical images can be considered as almost ideal two-dimensional projection images, similar to images obtained by computer tomography in medical applications. However, in cryo-EM the relative orientation of the molecules is a priori unknown and must be determined by computational means prior to calculating the 3D structure.

Cryo-EM is the method of choice for 3D structure determination of macromolecular complexes that are difficult to purify in the amounts and quality that is required for crystallization (X-ray crystallography). Due to the low copy number of many functionally important macromolecular complexes in the cell, cryo-EM is very often the only available method to study the 3D structure of these large macromolecules. Work in our group concentrates on macromolecular complexes related to pre-mRNA splicing, translation and cell cycle regulation and on the development of new methods to improve sample preparation, imaging and computational image processing techniques

Selected Recent Publications

Fischer N, Neumann P, Konevega AL, Bock LV, Ficner R, Rodnina MV, Stark H (2015) Structure of the *E. coli* ribosome-EF-Tu complex at <3 Å resolution by Cs-corrected cryo-EM. Nature 520(7548):567-70

Chari A, Haselbach D, Kirves JM, Ohmer J, Paknia E, Fischer N, Ganichkin O, Möller V, Frye JJ, Petzold G, Jarvis M, Tietzel M, Grimm C, Peters JM, Schulman BA, Tittmann K, Markl J, Fischer U, Stark H (2015) ProteoPlex: stability optimization of macromolecular complexes by sparse-matrix screening of chemical space. Nat Methods 12(9):859-65

Hauer F, Gerle C, Fischer N, Oshima A, Shinzawa-Itoh K, Shimada S, Yokoyama K, Fujiyoshi Y, Stark H (2015) GraDeR: Membrane Protein Complex Preparation for Single-Particle Cryo-EM. Structure 23(9):1769-75

Martinez-Rucobo FW, Kohler R, van de Waterbeemd M, Heck AJ, Hemann M, Herzog F, Stark H, Cramer P (2015) Molecular Basis of Transcription-Coupled Pre-mRNA Capping. Mol Cell 8(6):1079-89

Fischer N, Konevega AL, Wintermeyer W, Rodnina MV, Stark H (2010) Ribosome dynamics and tRNA movement as visualized by time-resolved electron cryomicroscopy. Nature 466: 329-333

Herzog F, Primorac I, Dube P, Lenart P, Sander B, Mechtler K, Stark H, Peters JM (2009) Structure of the anaphase-promoting complex/cyclosome interacting with a mitotic checkpoint complex. Science 323: 1477-1481

Address

Institute for Organic and Biomolecular Chemistry
University of Göttingen
Tammannstr. 2

37077 Göttingen
Germany

phone: +49-551-39 33294
fax: +49-551-39 33228
e-mail: csteine@gwdg.de

Further Information

http://www.uni-goettingen.de /de/213067.html

Claudia Steinem

- 1987 – 1989 Studies of Biology at the University of Münster
- 1989 – 1994 Studies of Chemistry at the University of Münster
- 1994 – 1997 PhD thesis under supervision of Prof. Dr. H.-J. Galla
- 1997 – 1998 Postdoctoral Researcher at the Scripps Research Institute (La Jolla, California, USA)
- 1999 – 2001 Habilitation in Biochemistry at the University of Münster
- 2001 – 2006 Associate professor (C3) for Bioanalytics and Biosensors at the University of Regensburg
- 2006 Full professor (W3) for Biomolecular Chemistry at the University of Göttingen

Major Research Interests

Development and application of new artificial membrane systems based on highly ordered porous substrates; transport processes across membranes; protein-membrane and protein-cytoskeleton interactions; membrane fusion and –fission; membrane-confined silica formation in diatoms.

Selected Recent Publications

Schwenen LLG, Hubrich R, Milovanovic D, Geil B, Yang J, Kros A, Jahn R, Steinem C (2015) Resolving single membrane fusion events on planar pore-spanning membranes. Sci Rep 5: 12006

Schütte OM, Ries A, Orth A, Patalag LK, Römer W, Steinem C, Werz DB (2014) Influence of Gb3 glycosphingolipids differing in their fatty acid chain on the phase behavior of solid supported membranes: Chemical syntheses and impact of Shiga toxin binding. Chem Sci 5: 3104-3114

Braunger J A, Brückner BR, Nehls S, Pietuch A, Gerke V Mey I, Janshoff A, Steinem C (2014) Phosphatidylinositol 4,5-bisphosphate alters the number of attachment sites between ezrin and actin filaments: a colloidal probe study. J Biol Chem 289: 9833-9843

Gleisner M, Mey I, Barbot M, Dreker C, Meinecke M, Steinem C (2014) Driving a planar model system into the 3rd dimension: Generation and control of curved pore-spanning membrane arrays. Soft Matter 10: 6228-6236

Neubacher H, Carnarius C, Mey I, Lazzara TD, Steinem C (2014) Permeabilization assay for antimicrobial peptides based on pore-spanning lipid membranes on nanoporous alumina. Langmuir 30: 4767-4774

Kozuch J, Weichbrodt C, Millo D, Becker S, Giller K, Hildebrandt P, Steinem C (2014) Voltage-dependent structural changes of the membrane-bound anion channel hVDAC1 probed by SEIRA and electrochemical impedance spectroscopy. Phys Chem Chem Phys 16: 9546-9555

Song C, Weichbrodt C, Salnikovc ES, Dynowskid M, Forsberg BO, Bechinger B, Steinem C, de Groot BL, Zachariae U, Zeth K (2013) Crystal structure and functional mechanism of a human antimicrobial membrane channel. Proc Natl Acad Sci USA 110: 4586-4591

Lazzara T D, Carnarius C, Kokun M, Janshoff A, Steinem C (2011) Separating attoliter-sized compartments using fluid pore-spanning lipid bilayers. ACS Nano 5: 6935–6944

Bosk S, Braunger J, Gerke V, Steinem C (2011) Activation of F-actin binding capacity of ezrin: synergism of PIP2 interaction and phosphorylation. Biophys J 100: 1708-1717

Bernecker A, Wieneke R, Riedel R, Seibt M, Geyer A, Steinem C (2010) Tailored synthetic polyamines for controlled biomimetic silica formation. J Am Chem Soc 132: 1023-1031

Address

Department of General Microbiology
University of Göttingen
Grisebachstr. 8

37077 Göttingen
Germany

phone: +49-551-39 33781
fax: +49-551-39 33808
e-mail: jstuelk@gwdg.de

Further Information

http://genmibio.uni-goettingen.de/

Jörg Stülke

Professor of Microbiology

- 1990 Diploma (Biology), Ernst-Moritz-Arndt-Universität Greifswald
- 1994 Dissertation (Dr. rer. nat.), Ernst-Moritz-Arndt-Universität Greifswald
- 1994 – 1996 Postdoctoral Fellow at the Institut Pasteur, Paris
- 1996 – 2003 Group leader at the Chair of Microbiology, University Erlangen-Nürnberg
- 2000 Habilitation (Microbiology), University Erlangen-Nürnberg
- Since 2003 Professor of General Microbiology, Head of the Department of General Microbiology at the Institute of Microbiology and Genetics, University of Göttingen

Major Research Interests

Our group studies the regulation of metabolism in the pathogenic bacterium *Mycoplasma pneumoniae* and the model organism *Bacillus subtilis*. We are following global ("post-genomic") and gene-specific approaches. In *Mycoplasma pneumoniae*, we study the regulation of gene expression in this pathogenic bacterium and its relation to pathogenicity. This is highly interesting because this bacterium is an important cause of pneumonia. Moreover, *M. pneumoniae* is one of the organisms with the smallest genetic equipment that is capable of independent life. Understanding *M. pneumoniae* means understanding life! Specifically, we are analysing protein phosphorylation and mechanisms of transcription regulation in *M. pneumoniae*. We have shown, that protein phosphorylation of is of key importance for pathogenicity of *M. pneumoniae*. Metabolism in *Bacillus subtilis* is studied by transcriptomics, metabolome and fluxome analyses. Our specific interests are focussed on two key pathways: glycolysis and glutamate biosynthesis, the decisive link between carbon and nitrogen metabolism. The regulation of glycolysis is studied at the level of a controlled protein-RNA interaction. Regulation through RNA has become widely recognized in the past few years. Our studies revealed that glycolytic enzymes themselves are part of a protein complex that is required for mRNA processing and degradation. Finally, we are interested in systems biology approaches to the analysis of *B. subtilis* and develop web interfaces for the functional annotation.

Selected Recent Publications

Michna RH, Zhu B, Mäder U, Stülke J (2015) SubtiWiki 2.0-an integrated database for the model organism *Bacillus subtilis*. Nucleic Acids Res [Epub ahead of print]

Kampf J, Stülke J. Minor Cause--Major Effect: A Novel Mode of Control of Bistable Gene Expression (2015) PLoS Genet 11(6):e1005229

Michna RH, Commichau FM, Tödter D, Zschiedrich CP, Stülke J (2014) SubtiWiki – a database for the model organism *Bacillus subtilis* that links pathway, interaction, and expression information. Nucleic Acids Res 42: D692-D698

Mehne FM, Schröder-Tittmann K, Eijlander RT, Herzberg C, Hewitt L, Kaever V, Lewis RJ, Kuipers OP, Tittmann K, Stülke J (2014) Control of the diadenylate cyclase CdaS in *Bacillus subtilis*: an autoinhibitory domain limits cyclic di-AMP production. J Biol Chem 289(30):21098-107

Rothe FM, Bahr T, Stülke J, Rak B, Görke B (2012) Activation of *Escherichia coli* antiterminator BglG requires its phosphorylation. Proc Natl Acad Sci USA 109: 15906-15911

Nicolas P, Mäder U, Dervyn E, …, Stülke J …, Völker U, Bessières P, Noirot P (2012) The condition-dependent whole-transcriptome reveals high-level regulatory architecture in bacteria. Science 335: 1103-1106

Görke B, Stülke J (2008) Carbon catabolite repression in bacteria: many ways to make most out of nutrients. Nature Rev Microbiol 6: 613-624

Address

Dept. of Cellular Biochemistry
University Medical Center Göttingen
Humboldtallee 23

37073 Göttingen
Germany

phone: +49-551-39 5958
fax: +49-551-39 5979
e-mail: mthumm@uni-goettingen.de

Michael Thumm

Professor of Biochemistry and Molecular Cell Biology

- Center of Biochemistry and Molecular Cell Biology, University of Göttingen
- 1987 Dr. rer. nat., University of Stuttgart
- 1997 Habilitation (Biochemistry), University of Stuttgart

Major Research Interests

We are studying the molecular mechanism of autophagy in the yeast *Saccharomyces cerevisiae*. Autophagy is a starvation induced transport pathway, which delivers cytosolic material for degradation to the lysosome (vacuole). It is highly conserved in all eukaryotes from yeast to human and helps the cells to survive periods of nutrient limitation.

Autophagy further plays an important role in ageing, the development of breast cancer and cardiomyopathy and it was linked to neurodegenerative diseases like Alzheimer´s, Huntington´s and Parkinson´s disease. Autophagy is mechanistically unique, since its transport intermediates, the autophagosomes, are surrounded by two individual membranes. It starts at the newly-discovered preautophagosomal structure, where autophagosomes are formed. Autophagosomes unspecifically enclose parts of the cytoplasm including organelles like mitochondria, peroxisomes and parts of the ER.

When the autophagosomes reach the vacuole, their outer membrane-layer fuses with the vacuolar membrane and a still membrane-enclosed autophagic body is released into the vacuolar lumen. In the vacuole autophagic bodies are lysed and broken down together with their cytosolic content. The intravacuolar breakdown of autophagic bodies requires the selective lysis of their limiting membrane. Due to the use of two limiting membranes the biogenesis of autophagosomes is a very unique process. Molecular dissection of this process is one of our main areas of research.

Selected Recent Publications

Juris L, Montino M, Rube P, Schlotterhose P, Thumm M*, Krick R (2015). PI3P binding by Atg21 organises Atg8 lipidation. EMBO J 34(7): 955-973, *corresponding author

Thumm M, Simons M (2015) Myelinophagy: Schwann cells dine in. J Cell Biol 210(1): 9-10

Krick R, Busse RA, Scacioc A, Stephan M, Janshoff A, Thumm M, Kühnel K (2012) Structural and functional characterization of the two phosphoinositide binding sites of PROPPINs, aβ-propeller protein family. Proc Natl Acad Sci USA 109: E2042–9

Nair U, Thumm M*, Klionsky DJ*, Krick R (2011) GFP-Atg8 protease protection as a tool to monitor autophagosome biogenesis. Autophagy 7(12): 1546-1550, Toolbox, *corresponding authors

Krick R, Bremer S, Welter E, Schlotterhose P, Muehe Y, Eskelinen E-L, Thumm M (2010) Cdc48/p97 and Shp1/p47 regulate autophagosome biogenesis in concert with ubiquitin-like Atg8. J Cell Biol 190(6): 965-973

Welter E, Thumm M*, Krick R (2010) Quantification of nonselective bulk autophagy in S. cerevisiae using Pgk1-GFP. Autophagy (6): 794-7, Toolbox, *corresponding author

Krick R, Muehe Y, Prick T, Bremer S, Schlotterhose P, Eskelinen E-L, Millen J, Goldfarb DS, Thumm M (2008) Piecemeal microautophagy of the nucleus requires the core macroautophagy genes. Mol Biol Cell (19): 4492-4505

Krick R, Henke S, Tolstrup J, Thumm M (2008) Dissecting the localization and function of Atg18, Atg21 and Ygr223c. Autophagy 4(7): 896-905

Address

Dept. of Molecular Enzymology
Albrecht von Haller Institute
University of Göttingen
Justus-von-Liebig-Weg 11

37077 Göttingen
Germany

phone: +49-551-39 14430
fax: +49-551-39 5749
e-mail: ktittma@gwdg.de

Further Information

http://www.bioanalytik.uni-goettingen.de/

Kai Tittmann

Professor of Bioanalytics

- Diploma (Biochemistry), Martin-Luther-University, Halle/Saale (Germany), 1996
- Dr. rer. nat., Martin-Luther-University, Halle/Saale (Germany), 2000
- Postdoc, Institute for Biochemistry, MLU Halle-Wittenberg, Halle/Saale (Germany), 2001 – 2002
- Jun.-Prof. of Molecular Enzymology, Institute for Biochemistry, MLU Halle-Wittenberg, Halle/Saale, (Germany), 2003 – 2008
- Invited Research Scientist at Rutgers University, Newark, NJ, USA, 2003
- Associate Guest Professor, Ben-Gurion-University of the Negev, Beer-Sheva, IL, 2006
- Since 2008 Professor of Bioanalytics, Georg-August-University, Göttingen (Germany)
- Awards: Dorothea-Erxleben-Prize (best doctoral thesis), 2001
- Prize for excellent basic research at Saxony-Anhalt, 2005

Major Research Interests

The central research topic of our department is the analysis of molecular reaction mechanisms of enzymes as nature's chemical catalysts. In this context, we study enzymes with vitamin-derived cofactors, with metal ions, and Schiff base-forming enzymes. A particular focus is laid on the structural and kinetic characterization of enzymatic reaction intermediates by high-resolution X-ray crystallography, steady-state and transient kinetic methods, NMR spectroscopy and theoretical studies. Knowledge about the reaction mechanism is exploited to redesign enzymes for biocatalytic applications and for drug design.

Selected Recent Publications

Sautner V, Friedrich MM, Lehwess-Litzmann A, Tittmann K (2015) Converting Transaldolase into Aldolase through Swapping of the Multifunctional Acid-Base Catalyst: Common and Divergent Catalytic Principles in F6P Aldolase and Transaldolase. Biochemistry 54(29):4475-86

Brodhun F, Tittmann K (2015) Membrane enzymes: transformers at the interface. Nat Chem Biol 11(2):102-3

Neumann P, Tittmann K (2014) Marvels of enzyme catalysis at true atomic resolution: distortions, bond elongations, hidden flips, protonation states and atom identities. Curr Opin Struct Biol 29:122-33

Schröder-Tittmann K, Meyer D, Arens J, Wechsler C, Tietzel M, Golbik R, Tittmann K (2013) Alternating sites reactivity is a common feature of thiamin diphosphate-dependent enzymes as evidenced by isothermal titration calorimetry studies of substrate binding. Biochemistry 52(15):2505-7

Lüdtke S, Neumann P, Erixon KM, Leeper F, Kluger R, Ficner R, Tittmann K (2013) Sub-Angström resolution crystallography reveals physical distortions that enhance reactivity of a covalent enzymatic intermediate. Nature Chem 5: 762-767

Meyer D, Neumann P, Ficner R, Tittmann K (2013) Observation of a stable carbene at the active site of a thiamin enzyme. Nature Chem Biol 9: 488-490

Meyer D, Neumann P, Koers E, Sjuts H, Lüdtke S, Sheldrick, GM, Ficner R, Tittmann K (2012) Unexpected tautomeric equilibria of the carbanion-enamine intermediate in pyruvate oxidase highlight unrecognized chemical versatility of the thiamin cofactor. Proc Natl Acad Sci USA 109(27): 10867-72

Lehwess-Litzmann A, Neumann P, Parthier C, Lüdtke S, Golbik R, Ficner R, Tittmann K (2011) Twisted Schiff-base Intermediates and Substrate Locale Revise Transaldolase Mechanism. Nature Chem Biol 7: 678-684

Address

Bioanalytical Mass Spectrometry Group
Max Planck Institute for Biophysical Chemistry
Am Fassberg 11

37077 Göttingen
Germany

phone: +49-551-201 1060
fax: +49-551-201 1197
e-mail: henning.urlaub@mpi-bpc.mpg.de

University Medical Center Goettingen
Bioanalytics
Department of Clinical Chemistry
Robert Koch Strasse 40

37075 Göttingen
Germany

phone: +49-551-39 6160
fax: +49-551-39 8551
e-mail: henning.urlaub@med.uni-goettingen.de

Further Information

http://www.mpibpc.gwdg.de/english/research/ags/urlaub/index.html

Henning Urlaub

Group Leader - Bioanalytical Mass Spectrometry Group

- from 2010: Group leader “Bioanalytical Mass Spectrometry” group at the Max Planck Institute for Biophysical Chemistry, Göttingen and “Bioanalytics” group at University Medical Center Göttingen (UMG) within Dept. of Clinical Chemistry
- 2010: Professor at the Faculty of Medicine at Georg August University Göttingen
- 2005: Research group “Bioanalytical Mass Spectrometry Group” at the Max Planck Institute for Biophysical Chemistry
- 2001: Responsibility for running the mass spectrometry unit in the Dept. of Cellular Biochemistry at the Max Planck Institute for Biophysical Chemistry in Göttingen
- 2000 – 2001: Guest researcher at the EMBL in Heidelberg, Germany, in the group of Dr. Matthias Wilm
- 1997 – 2001: Post-Doc at the “Institut für Molekularbiologie und Tumorforschung” (IMT) of the Philipps University of Marburg, Germany (Group of Reinhard Lührmann) and at the Max Planck Institute for Biophysical Chemistry in Göttingen (Group of Reinhard Lührmann)
- 1993 – 1996 Ph.D. and Post-Doc in the research group of Prof. Brigitte Wittmann-Liebold at the Max Delbrück Center for Molecular Medicine (MDC) in Berlin
- 1992 – 1993 Diploma thesis in the research group of Prof. Volker A.
- Erdmann at the Institute of Biochemistry of the Free University of Berlin
- 1987 – 1993 Studied biochemistry at the Free University of Berlin, Germany

Major Research Interests

Modern mass-spectrometric methods have become key technologies in the life sciences. We apply “state-of-the-art” mass spectrometry to elucidate quantitative changes of proteins and their post-translational modifications derived from different samples, including tissue, cells, organelles, and cell compartments. In addition we apply mass spectrometric methods to monitor dynamic changes of protein and protein-ligand complexes through use of crosslinking and chemical probing. In this respect, we collaborate with several groups within the GGNB, like the groups of Wolfgang Fischle, Dirk Görlich, Reinhard Jahn, Reinhard Lühr-mann, Peter Rehling, Oliver Schlüter, Holger Stark, Jürgen Wienands, Markus Zweckstetter, and many others. We provide solutions and analytical workflows for solving cell biological issues; we further develop novel analytical workflows for in-depth analyses of entire proteomes and for structural analyses of proteins.

Selected Recent Publications

Zaman U, Richter FM, Hofele R, Kramer K, Sachsenberg T, Kohlbacher O, Lenz C, Urlaub H (2015) Dithiothreitol (DTT) acts as a specific, UV-inducible cross-linker in elucidation of protein-RNA interactions. Mol Cell Proteomics [Epub ahead of print]

Sharma K, Hrle A, Kramer K, Sachsenberg T, Staals RH, Randau L, Marchfelder A, van der Oost J, Kohlbacher O, Conti E, Urlaub H (2015) Analysis of protein-RNA interactions in CRISPR proteins and effector complexes by UV-induced cross-linking and mass spectrometry. Methods 89: 138-48

Kramer K, Sachsenberg T, Beckmann BM, Qamar S, Boon KL, Hentze MW, Kohlbacher O, Urlaub H (2014) Photo-cross-linking and high-resolution mass spectrometry for assignment of RNA-binding sites in RNA-binding proteins. Nat Methods 11(10): 1064-70

Schmidt C, Grønborg M, Deckert J, Bessonov S, Conrad T, Lührmann R, Urlaub H (2014) Mass spectrometry-based relative quantification of proteins in precatalytic and catalytically active spliceosomes by metabolic labeling (SILAC), chemical labeling (iTRAQ), and label-free spectral count. RNA 20(3): 406-20

Address

Dept. of Primate Genetics
German Primate Center
Kellnerweg 4

37077 Göttingen
Germany

phone: +49-551-3851 161
fax: +49-551-3851 228
e-mail: lwalter@gwdg.de

Further Information

http://dpz.eu/index.php?id=86

Lutz Walter

Head of Department of Primate Genetics at the German Primate Center

- Dr. rer. nat. (PhD), University of Göttingen, 1994
- Postdoctoral fellow and group leader at the Division of Immunogenetics, University of Göttingen, 1994 – 2004
- Head of Department of Primate Genetics, German Primate Center, Göttingen, since 2004
- Habilitation (Immunology and Immunogenetics), Medical Faculty of the University of Göttingen, 2005
- apl Professor, Medical Faculty of the University of Göttingen, 2009

Major Research Interests

Natural killer (NK) cells belong to the lymphocyte lineage and represent an essential part of the innate immune system. NK cells can kill other cells and secrete substantial amounts of cytokines. Signals from activating and inhibitory NK cell receptors are integrated and regulate the activity of NK cells. Typical targets for NK cell killing are virus-infected or malignant cells, which both frequently reveal changed patterns of ligand expression on their cell surface. Such changes are recognised by NK cells, leading to killing of virally infected or transformed cells. NK cells can also be activated by different stimuli during interaction with dendritic cells, leading to release of pro-inflammatory cytokines and anti-viral substances. Due to these properties, NK cells play also important roles in autoimmune diseases, transplantation, and reproduction. Recently, NK cells were shown to possess immunological memory. Our interests lie in biology and genetics of natural killer (NK) cells, including regulation of NK cell receptor gene transcription, specific interactions of NK cell receptors and MHC class I ligands, and regulation of NK cell activation.
A further focus of our research is genomics of nonhuman primates with phylogenetic and evolutionary analyses.
Methods: single-cell RNA sequencing, single-cell qRT-PCR, flow cytometry, next-generation sequencing, bioinformatic analysis tools

Selected Recent Publications

Walter L, Ansari AA (2015) MHC and KIR Polymorphisms in Rhesus Macaque SIV Infection. Front Immunol 6:540

Carbone et al. (2014) Gibbon genome and the fast karyotype evolution of small apes. Nature 513: 195-201

Albrecht C, Malzahn D, Brameier M, Hermes M, Ansari AA, Walter L (2014) Progression to AIDS in SIV-infected rhesus macaques is associated with distinct KIR and MHC class I polymorphisms and NK cell dysfunction. Front Immunol 5: 600

Byrareddy SN, Kallam B, Arthos J, Cicala C, Nawaz F, Hiatt J, Kersh EN, McNicholl JM, Hanson D, Reimann KA, Brameier M, Walter L, Rogers K, Mayne AE, Dunbar P, Villinger T, Little D, Parslow TG, Santangelo PJ, Villinger F, Fauci AS, Ansari AA (2014) Blockade of alpha4beta7 integrin, a T-cell gut-homing receptor, reduces mucosal transmission and dissemination of simian immunodeficiency virus infection. Nat Med 20: 1397-1400

Walter L (2014): Immunogenetics of NK cell receptors and MHC class I ligands in non-human primates. In: Ansari AA, Silvestri G (eds) Natural hosts of SIV. Implications in AIDS. Elsevier, pp. 269-285

Address

Dept. of Cellular and Molecular Immunology
University Medical Center Göttingen
Humboldtallee 34

37073 Göttingen
Germany

phone: +49-551-39 5812
fax: +49-551-39 5843
e-mail: jwienan@uni-goettingen.de

Further Information

http://www.immunologie.uni-goettingen.de

Jürgen Wienands

Professor of Cellular and Molecular Immunology

- 1982 – 89 Study of Biology at the University of Cologne; graduated at the Institute of Genetics, Dept. of Immunology
- 1989 – 92 Ph.D. poject at the Max Planck Institute for Immunobiology, Freiburg, Germany
- 1992 – 94 Postdoctoral fellow at the Dept. of Preclinical Research at Sandoz Pharma Ltd., Basel, Switzerland
- 1994 – 96 Postdoctoral fellow at the Max Planck Institute for Immunobiology, Freiburg, Germany
- 1996 – 2001 Group leader at the University of Freiburg, Institute of Biology III
- 2001 “Habilitation” and Venia Legendi in “Molecular Immunology and Biochemistry”
- 2001 – 2004 Full Professor for “Biochemistry and Molecular Immunology” at the University of Bielefeld
- since August 2004 Full Professor for “Molecular and Cellular Immunology” at the University of Göttingen

Major Research Interests

The signature structure of B lymphocytes is their clonotypic antigen receptor (BCR), which recognizes extracellular pathogens or toxins, and consequently initiates their combating by soluble antibodies. Our research focuses on how the ligated BCR activates intracellular signaling pathways upon primary and secondary antigen encounter. Our studies showed that BCR classes expressed on antigen-experienced, so-called memory B cells, possess a signal amplification mechanism that lowers the BCR signaling threshold compared to newly generated B cells. This finding provides a molecular explanation for immunological memory which is the fundamental basis for successful vaccination strategies. We also identified key effector proteins of the BCR such as SLP-65 or CIN85. They function as adaptor proteins which nucleate the formation of multi-molecular protein complexes to integrate and amplify BCR signals. Interference with expression or function of these effectors cause severe immunodeficiencies in mouse and man. To investigate these processes we apply cutting edge technologies of biochemistry and genetics including protein interaction studies, flow cytometry, targeted gene disruption in cell culture and embryonic stem cells followed by reconstitution experiments using electroporation techniques or retroviral gene transfer

Selected Recent Publications

Engelke M, Pirkuliyeva S, Kühn J, Wong L, Boyken J, Herrmann N, Becker S, Griesinger C, Wienands J (2014) Macromolecular assembly of the adaptor SLP-65 at intracellular vesicles in resting B cells. Sci Signal 7: 339

Oellerich T, Bremes V, Neumann K, Dittmann K, Bohnenberger H, Engelke M, Hsiao HH, Schneyder T, Batista FD, Urlaub H, Wienands J (2011) The B cell antigen receptor signals through a preformed transducer module of SLP65 and CIN85. EMBO J 30: 3620-363

Engels N, König L, Heemann C, Lutz J, Tsubata T, Griep S, Schrader V, Wienands J (2009) Recruitment of the cytoplasmic adapter Grb2 to surface IgG and IgE provides antigen receptor-intrinsic costimulation to class-switched B cells. Nature Immunol 10: 1018-1025

Stork B, Neumann K, Goldbeck I, Alers S, Kähne T, Naumann M, Engelke M, Wienands J (2007) Subcellular localization of Grb2 by the adaptor protein Dok-3 restricts the intensity of Ca^{2+} signaling in B cells. EMBO J 26: 1140-1149

for review see:

Engels N and Wienands J (2011) The signaling tool box for tyrosine-based costimulation of lymphocytes. Curr Opin Immunol 23: 324-329

Address

Dept. of Developmental Biology
Johann-Friedrich-Blumenbach-Institute of Zoology and Anthropology
Georg-August-University Göttingen
GZMB, Ernst-Caspari-Haus
Justus-von-Liebig-Weg 11

37077 Göttingen
Germany

phone: +49-551-39 22889
fax: +49-551-39 5416
e-mail: ewimmer@gwdg.de

Further Information

http://www.uni-goettingen.de/en/sh/49202.html

Ernst Wimmer

Professor of Developmental Biology

- 1991 Diplom (Biology), Ludwig Maximilians University, Munich (Germany)
- 1995 Dr. rer. nat., Max-Planck-Institute for Biophysical Chemistry, Göttingen (Germany) and Howard Hughes Medical Institute, Baylor College of Medicine, Houston (USA)
- 1995 – 1998 Postdoctoral Fellow and Associate, Howard Hughes Medical Institute, The Rockefeller University, New York (USA)
- 1998 – 2003 Assistant Professor and Robert Bosch Foundation 'Junior Professor' Department of Genetics, University of Bayreuth, Bayreuth (Germany)
- Since 2003 Professor of Developmental Biology at the Johann Friedrich Blumenbach Institute of Zoology and Anthropology, Georg August University, Göttingen (Germany)

Major Research Interests

Phylogenetic Variance and Plasticity of Developmental Processes. A key question in evolutionary developmental biology is how diverse animal body plans are specified. To identify the plasticity in developmental processes, we study their conservation and divergence in different arthropod species by transgenesis and functional genomics approaches. This will help us to understand how animal evolution is based on changes in gene regulation governing pattern formation processes.
Smelling Beetles: Stink Glands and Odour Detection the Red Flour Beetle *Tribolium castaneum*. Beetles are prolific producers of repellent and/or toxic compounds. Defensive substances are usually multifunctional: as repellents, toxicants, insecticides, or antimicrobics, they are directed against a large array of potential target organisms or may function for boiling bombardment or as surfactants. We are interested both in the development of these glands as well as their biochemical composition and biological function. The red flour beetle also offers a great system to address olfaction from the odour recognition and discrimination at the periphery to the analysis of the plasticity of the central olfactory pathway. Our focus lays on the biological function of odorant binding proteins (OBPs) and sensory neuron membrane proteins (SNMPs) which is still largely unknown, despite their necessity for olfaction.
Applied Developmental Biology. Biotechnological improvements on the Sterile Insect Technique (SIT). SIT is a successful genetic pest management strategy to prevent, control, suppress, or even eradicate invasive insect pest species from islands, large agricultural production areas, or even complete continents. SIT is a species-specific and eco-friendly insect birth control measure involving mass production, sterilization, and sustained area-wide release of large quantities of sterilized insects. This leads to unproductive matings, which shrinks the population. Our current biotechnological efforts improve on transgenic female-specific lethality systems to enable more efficient male-only releases, on reproductive sterility systems to overcome the problem of radiation-reduced fitness, and on transgenic markers to better monitor the efficacy of SIT applications.

Selected Recent Publications

Schmitt-Engel C, et al. (2015) The iBeetle large scale RNAi screen reveals novel gene functions for insect development and physiology. Nat Commun 6: 7822

Dippel S, Oberhofer G, Kahnt J, Gerischer L, Opitz L, Schachtner J, Stanke M, Schütz S, Wimmer EA* Angeli S (2014) Tissue-specific transcriptomics, chromosomal localization, and phylogeny of chemosensory and odorant binding proteins from the red flour beetle Tribolium castaneum reveal subgroup specificities for olfaction or more general functions. BMC Genomics 15: 1141, * corresponding author

Li J, Lehmann S, Weißbecker B, Ojeda-Naharros I, Schütz S, Joop G, Wimmer EA (2013) Odoriferous defensive stink gland transcriptome to identify novel genes for quinone synthesis in the red flour beetle, *Tribolium castaneum*. PLoS Genet 9, e1003596

Ogaugwu CE, Schetelig MF, Wimmer EA (2013) Transgenic sexing system for *Ceratitis capitata* (Diptera: Tephritidae) based on female-specific embryonic lethality. Insect Biochem Mol Biol 43, 1-8

Schetelig MF, Caceres C, Zacharopoulou A, Franz G, Wimmer EA (2009) Conditional embryonic lethality to improve the sterile insect technique in *Ceratitis capitata* (Wiedemann; Diptera: Tephritidae). BMC Biology 7: 4

Schetelig MF, Scolari F, Kittelmann S, Malacrida AR, Gasperi G, Wimmer, EA (2009) Site-specific integration to modify successfully tested transgenic *Ceratitis capitata* (Diptera: Tephritidae) lines. Proc Natl Acad Sci USA 106: 18171-6

Graduate Program Committee

Faculty

Prof. Dr. Peter Rehling (Chair)
Prof. Dr. Jörg Stülke (Vice Chair)
Prof. Dr. Marina Rodnina (Dean)
Prof. Dr. Claudia Höbartner
Prof. Dr. Stefanie Pöggeler
PD Dr. Wilfried Kramer

Students

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Students

Kora Richter
Jana Kroll

Program Coordination

Molecular Biology Program

Dr. Steffen Burkhardt
(Program Coordinator)

Kerstin Grüniger
(Program Assistant)

Georg-August-Universität
Göttingen
Coordination Office
Molecular Biology
Justus-von-Liebig-Weg 11

37077 Göttingen
Germany

phone:
+49 – 551 – 39 12110 / 12111
fax:
+49 – 551 – 39 33811
e-mail:
gpmolbio@gwdg.de

Further Information

http://www.gpmolbio.uni-goettingen.de

Neuroscience Program

Prof. Dr. Michael Hörner
(Program Coordinator)

Sandra Drube
(Program Assistant)

Imprint

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Dr. Steffen Burkhardt,

Prof. Dr. Michael Hörner

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Georg-August-Universität
Göttingen

Max Planck Institutes for
- Biophysical Chemistry
- Experimental Medicine

DPZ

German
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GZMB

Göttingen Center
for Molecular Biosciences

www.gpmolbio.uni-goettingen.de